

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 29, 2006, 01:38:52 ; Search time 124.25 Seconds
(without alignments)
49.507 Million cell updates/sec

Title: US-10-712-447-210
Perfect score: 20
Sequence: 1 XXRRXXXXXXXXX 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 21.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*
9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	95.0	133	7 ABO73099	Abo73099 Pseudomon
2	19	95.0	189	7 ABO83630	Abo83630 Pseudomon
3	19	95.0	323	8 ADX97192	Adx97192 Plant ful
4	19	95.0	442	7 ABO74539	Abo74539 Pseudomon
5	19	95.0	533	5 ADH48840	Adh48840 NOV53 pro
6	19	95.0	534	7 ADG48250	Adg48250 Human ret
7	19	95.0	644	4 AAU33234	Aau33234 Novel hum
8	19	95.0	19938	6 ABP76678	Abp76678 Streptomy
9	18	90.0	15	5 AAB71432	Aab71432 Peptide A
10	18	90.0	16	5 AAB71430	Aab71430 Peptide T
11	18	90.0	19	3 AAY87840	Aay87840 Heparin b
12	18	90.0	19	5 AAB71428	Aab71428 Peptide B
13	18	90.0	59	5 ABP00279	Abp00279 Human ORF
14	18	90.0	64	8 ADX75905	Adx75905 Plant ful
15	18	90.0	77	4 AAU41918	Aau41918 Propionib
16	18	90.0	77	6 ABM38437	Abm38437 Propionib
17	18	90.0	78	5 ABP00666	Abp00666 Human ORF
18	18	90.0	89	4 AAU52059	Aau52059 Propionib
19	18	90.0	89	6 ABM58578	Abm58578 Propionib
20	18	90.0	93	5 ABP05425	Abp05425 Human ORF
21	18	90.0	103	7 ABO83790	Abo83790 Pseudomon
22	18	90.0	113	7 ABO68429	Abo68429 Pseudomon
23	18	90.0	127	4 AAU86821	Aau86821 Novel hum
24	18	90.0	127	7 ADB60155	Adb60155 Connectiv

25	18	90.0	134	7 ABO72505	Abo72505 Pseudomon
26	18	90.0	136	8 ADX87688	Adx87688 Plant ful
27	18	90.0	139	7 ABO78160	Abo78160 Pseudomon
28	18	90.0	139	7 ABO75935	Abo75935 Pseudomon
29	18	90.0	140	8 ADX78723	Adx78723 Plant ful
30	18	90.0	141	7 ABO74930	Abo74930 Pseudomon
31	18	90.0	142	7 ABO82700	Abo82700 Pseudomon
32	18	90.0	143	6 ABU11486	Abu11486 Human MDD
33	18	90.0	149	4 AAU42224	Aau42224 Propionib
34	18	90.0	149	6 ABM38743	Abm38743 Propionib
35	18	90.0	152	7 ABO76573	Abo76573 Pseudomon
36	18	90.0	190	8 ADX93670	Adx93670 Plant ful
37	18	90.0	207	7 ABO73028	Abo73028 Pseudomon
38	18	90.0	208	7 ABO68892	Abo68892 Pseudomon
39	18	90.0	209	7 ABO72617	Abo72617 Pseudomon
40	18	90.0	229	4 AAU47602	Aau47602 Propionib
41	18	90.0	229	6 ABM44121	Abm44121 Propionib
42	18	90.0	231	7 ABO68472	Abo68472 Pseudomon
43	18	90.0	237	7 ABO83595	Abo83595 Pseudomon
44	18	90.0	245	4 AAG90194	Aag90194 C glutami
45	18	90.0	255	8 ADY11827	Ady11827 Plant ful

ALIGNMENTS

RESULT 1
ABO73099
ID ABO73099 standard; protein; 133 AA.
XX AC ABO73099;
XX XX
DT 29-JUL-2004 (first entry)
XX XX
DE Pseudomonas aeruginosa polypeptide #5274.
XX XX
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX OS Pseudomonas aeruginosa.
XX XX
PN US6551795-B1.
XX PD 22-APR-2003.
XX PF 18-FEB-1999; 99US-00252991.
XX PR 18-FEB-1998; 98US-0074788P.
XX PR 27-JUL-1998; 98US-0094190P.
XX (GENO-) GENOME THERAPEUTICS CORP.
XX PA Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX WPI; 2003-615309/58.
XX N-PSDB; ABD06670.
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX Disclosure; SEQ ID NO 21845; 455pp; English.
XX The invention relates to Pseudomonas aeruginosa polypeptides and the
XX polynucleotides encoding them. The sequences are useful in diagnosis and
XX therapy of pathological conditions, as molecular targets for diagnostics, and
XX prophylaxis and treatment of pathological conditions resulting from a
XX bacterial infection, for evaluating a compound, such as a polypeptide, of
XX for the ability to bind a P. aeruginosa nucleic acid, as components of
XX effective antibacterial targets, as targets for antibacterial drugs,
XX including anti-P. aeruginosa drugs, as templates for recombinant
XX production of P. aeruginosa-derived peptides or polypeptides, as target
XX components for diagnosis and/or treatment of P. aeruginosa-caused
XX infection, and in detection of P. aeruginosa sequences or other sequences

CC invention.
XX SQ Sequence 323 AA;
Query Match 95.0%; Score 19; DB 8; Length 323;
Best Local Similarity 33.3%; Pred. No. 3e+03; 8; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Mismatches 0; Mismatches 0;
QY 3 RXXXXXXXXX 14
DB 270 RRAASRSRTAR 281
RESULT 4
ABO74539
ID ABO74539 standard; protein; 442 AA.
XX AC ABO74539;
XX DT 29-JUL-2004 (first entry)
XX DE Pseudomonas aeruginosa polypeptide #6714.
XX KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX OS Pseudomonas aeruginosa.
XX PN US6551795-B1.
XX PD 22-APR-2003.
XX PF 18-FEB-1999; 99US-00252991.
XX PR 18-FEB-1998; 98US-0074788P.
XX PR 27-JUL-1998; 98US-0094190P.
XX PA (GENO-) GENOME THERAPEUTICS CORP.
XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX WPI; 2003-615309/58.
XX DR N-PSDB; ABD08110.
XX PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
XX PT useful as molecular targets for diagnostics, prophylaxis and treatment of
XX PT pathological conditions resulting from bacterial infection.
XX PS Disclosure; SEQ ID NO 23285; 455pp; English.
XX CC The invention relates to Pseudomonas aeruginosa polypeptides and the
XX CC polynucleotides encoding them. The sequences are useful in diagnosis and
XX CC therapy of pathological conditions, as molecular targets for diagnostics,
XX CC prophylaxis and treatment of pathological conditions resulting from a
XX CC bacterial infection, for evaluating a compound, such as a polypeptide,
XX CC for the ability to bind a P. aeruginosa nucleic acid, as components of
XX CC effective antibacterial targets, as targets for antibacterial drugs,
XX CC including anti-P. aeruginosa drugs, as templates for recombinant
XX CC production of P. aeruginosa-derived peptides or polypeptides, as target
XX CC components for diagnosis and/or treatment of P. aeruginosa-caused
XX CC infection, and in detection of P. aeruginosa sequences or other sequences
XX CC of Pseudomonas species using biochip technology. Sequences ABO67826-
XX CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
XX CC sequence data for this patent did not form part of the printed
XX CC specification but was obtained in electronic format from USPTO at
XX CC seqdata.uspto.gov/sequence.html
XX SQ Sequence 442 AA;
Query Match 95.0%; Score 19; DB 7; Length 442;
Best Local Similarity 33.3%; Pred. No. 3.9e+03;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 3 RXXXXXXXXX 14

Db 307 RRAASRSRTAR 318
RESULT 5
ADH48840
ID ADH48840 standard; protein; 533 AA.
XX AC ADH48840;
XX DT 25-MAR-2004 (first entry)
XX DE NOV53 protein sequence, SEQ ID 124.
XX KW Human; NOVX; atherosclerosis; hypertension; obesity; cancer; cytostatic;
XX KW hypotensive; antiarteriosclerotic; anorectic; gene therapy; NOV53;
XX KW protein-kinase-like protein; chromosome 20.
XX OS Homo sapiens.
XX PN WO200268652-A2.
XX PD 06-SEP-2002.
XX PF 26-FEB-2002; 2002WO-US005910.
XX PR 26-FEB-2001; 2001US-0271646P.
XX PR 27-FEB-2001; 2001US-0271840P.
XX PR 28-FEB-2001; 2001US-0272404P.
XX PR 28-FEB-2001; 2001US-0272405P.
XX PR 28-FEB-2001; 2001US-0272410P.
XX PR 28-FEB-2001; 2001US-0272414P.
XX PR 02-MAR-2001; 2001US-0272787P.
XX PR 02-MAR-2001; 2001US-0273048P.
XX PR 02-MAR-2001; 2001US-0273300P.
XX PR 16-MAR-2001; 2001US-0276401P.
XX PR 20-MAR-2001; 2001US-0278660P.
XX PR 30-MAR-2001; 2001US-0280039P.
XX PR 02-APR-2001; 2001US-0280818P.
XX PR 12-APR-2001; 2001US-0283443P.
XX PR 23-APR-2001; 2001US-0285754P.
XX PR 24-APR-2001; 2001US-0286096P.
XX PR 03-MAY-2001; 2001US-0288353P.
XX PR 17-MAY-2001; 2001US-0291703P.
XX PR 31-MAY-2001; 2001US-0294834P.
XX PR 20-JUN-2001; 2001US-0299695P.
XX PR 21-JUN-2001; 2001US-0299845P.
XX PR 05-JUL-2001; 2001US-0303242P.
XX PR 13-AUG-2001; 2001US-0311981P.
XX PR 16-AUG-2001; 2001US-0312858P.
XX PR 17-AUG-2001; 2001US-0313280P.
XX PR 29-AUG-2001; 2001US-0315614P.
XX PR 17-SEP-2001; 2001US-0322818P.
XX PR 25-FEB-2002; 2002US-00322818.
XX (CURA-) CURAGEN CORP.
XX PI Alsobrook JP, Anderson DW, Ballinger RA, Boldog FL, Burgess CE;
XX PI Casman SJ, Ellerman KE, Gangolli EA, Gerlach VL, Gilbert JA;
XX PI Gorman L, Guo X, Gusev VV, Kekuda R, Li L, Liu X, Malvankar UM;
XX PI Miller CE, Millet I, Padigar M, Patturajan M, Pena CE, Peyman JA;
XX PI Rastelli L, Shenoy SG, Shinkets RA, Smithson G, Spytek KA, Stone DJ;
XX PI Taupier RJ, Tchernev VT, Vernet CAM, Zernhusen BD;
XX WPI; 2002-698672/75.
XX DR N-PSDB; ADH48839.
XX PT New NOVX polypeptides or polynucleotides, useful for preventing or
XX PT treating disorders or syndromes e.g., atherosclerosis, hypertension,
XX PT obesity or cancer.

```

XX Claim 1; Page 298; 923pp; English.
XX
XX The present invention relates to novel human NOVX proteins, where X is
CC any number from 1 to 91 and their coding sequences. The proteins and
CC coding sequences are useful for preventing or treating disorders or
CC syndromes e.g. atherosclerosis, hypertension, obesity or cancer. NOV53 is
CC a protein kinase-like protein and its coding sequence maps to chromosome
CC 20.
XX
XX Sequence 533 AA;
SQ
    Query Match          95.0%; Score 19; DB 5; Length 533;
    Best Local Similarity 33.3%; Pred. No. 4.5e+03;
    Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 3 RRXXXXXXXRXR 14
Db 56 RRARAATRAAR 67
    |||
    |||

RESULT 6
ADG48250
ID ADG48250 standard; protein; 534 AA.
XX
XX ADG48250;
AC
XX
XX 11-MAR-2004 (first entry)
DT
XX
XX Human retina-specific protein kinase A203.
DE
XX
XX human; retina-specific protein; NET01; retinal disease;
KW age related macular degeneration; night blindness; protein kinase A203.
XX
XX Homo sapiens.
OS
XX
XX WO2003068967-A2.
PN
XX
XX 21-AUG-2003.
PD
XX
XX 18-FEB-2003; 2003WO-EP001625.
PF
XX
XX 18-FEB-2002; 2002EP-00003675.
PR
XX
XX 21-FEB-2002; 2002US-0357857P.
PR
XX
XX (LYNK-) LYNKEUS BIO TECH GMBH.
PA
XX
XX Stoehr BH, Weber FHB, Goehring F;
PI
XX
XX WPI; 2003-767334/72.
DR
XX
XX N-PSDB; ADG48249.
DR
XX
XX New nucleic acid encoding retinal protein sNET01, useful for diagnosis of
PT retinal disease, especially macular degeneration, also for drug screening
PT and therapy.
PT
XX
XX Claim 18; Fig 6; 199pp; English.
PS
XX
XX The invention comprises the amino acid and coding sequences of a human
CC retina-specific protein - NET01. The DNA and protein sequences of the
CC invention are useful in the treatment of retinal diseases, such as
CC macular degeneration (especially age related) and night blindness. The
CC present amino acid sequence represents human retina-specific protein
CC kinase A203.
CC
XX
XX Sequence 534 AA;
SQ
    Query Match          95.0%; Score 19; DB 7; Length 534;
    Best Local Similarity 33.3%; Pred. No. 4.5e+03;
    Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 3 RRXXXXXXXRXR 14
Db 56 RRARAATRAAR 67
    |||
    |||

Claim 1; Page 298; 923pp; English.

The present invention relates to novel human NOVX proteins, where X is
any number from 1 to 91 and their coding sequences. The proteins and
coding sequences are useful for preventing or treating disorders or
syndromes e.g. atherosclerosis, hypertension, obesity or cancer. NOV53 is
a protein kinase-like protein and its coding sequence maps to chromosome
20.

Sequence 533 AA;

Query Match          95.0%; Score 19; DB 5; Length 533;
Best Local Similarity 33.3%; Pred. No. 4.5e+03;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

3 RRXXXXXXXRXR 14
56 RRARAATRAAR 67
|||
|||

RESULT 6
ADG48250
ID ADG48250 standard; protein; 534 AA.
XX
XX ADG48250;
AC
XX
XX 11-MAR-2004 (first entry)
DT
XX
XX Human retina-specific protein kinase A203.
DE
XX
XX human; retina-specific protein; NET01; retinal disease;
KW age related macular degeneration; night blindness; protein kinase A203.
XX
XX Homo sapiens.
OS
XX
XX WO2003068967-A2.
PN
XX
XX 21-AUG-2003.
PD
XX
XX 18-FEB-2003; 2003WO-EP001625.
PF
XX
XX 18-FEB-2002; 2002EP-00003675.
PR
XX
XX 21-FEB-2002; 2002US-0357857P.
PR
XX
XX (LYNK-) LYNKEUS BIO TECH GMBH.
PA
XX
XX Stoehr BH, Weber FHB, Goehring F;
PI
XX
XX WPI; 2003-767334/72.
DR
XX
XX N-PSDB; ADG48249.
DR
XX
XX New nucleic acid encoding retinal protein sNET01, useful for diagnosis of
PT retinal disease, especially macular degeneration, also for drug screening
PT and therapy.
PT
XX
XX Claim 18; Fig 6; 199pp; English.
PS
XX
XX The invention comprises the amino acid and coding sequences of a human
CC retina-specific protein - NET01. The DNA and protein sequences of the
CC invention are useful in the treatment of retinal diseases, such as
CC macular degeneration (especially age related) and night blindness. The
CC present amino acid sequence represents human retina-specific protein
CC kinase A203.
CC
XX
XX Sequence 534 AA;
SQ
    Query Match          95.0%; Score 19; DB 7; Length 534;
    Best Local Similarity 33.3%; Pred. No. 4.5e+03;
    Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 3 RRXXXXXXXRXR 14
Db 56 RRARAATRAAR 67
    |||
    |||

RESULT 8
ABP76678
ID ABP76678 standard; protein; 19938 AA.
XX
XX ABP76678;
AC

```

XX 26-FEB-2003 (first entry)
DT Streptomyces viridochromogenes Avi gene cluster polypeptide frame 2.
DE
XX Avilamycin; antibacterial; virucide; protozoacide; fungicide; infection;
KW medicine; Staphylococcus aureus; biosynthetic gene cluster; enzyme.
KW
XX Streptomyces viridochromogenes.
OS
XX WO2000268436-A1.
PN
XX 06-SEP-2002.
PD
XX 24-AUG-2001; 2001WO-EP009815.
PF
XX 25-FEB-2001; 2001DE-01009166.
PR
XX (COMB-) COMBINATURE BIOPHARM AG.
PA
XX Weitnauer G, Muehlenweg A, Trefzer A, Bechthold A;
PI
XX WPI; 2003-018650/01.
XX N-PSDB; ABZ37515.
DR
XX New avilamycin derivatives, useful for treatment of infections, and
PT nucleic acid encoding avilamycin synthesis enzymes.
PT
XX Example 1; Page 68-301; 319pp; German.
PS
XX The invention relates to avilamycin derivatives (I) with antibacterial,
CC virucide, protozoacide and fungicide activity. (I) are useful for
CC treatment of infections (bacterial, viral, protozoal or fungal), in human
CC or veterinary medicine, particularly where caused by Staphylococcus
CC aureus. (I) are more hydrophilic than known avilamycins. The present
CC sequence is that of an avilamycin synthesis enzyme from the Streptomyces
CC viridochromogenes Avilamycin A biosynthetic gene cluster (ABZ37515-
XX ABZ37516)
XX
SQ Sequence 19938 AA;
Query Match 95.0%; Score 19; DB 6; Length 19938;
Best Local Similarity 33.3%; Pred. No. 7.6e+04;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 3 RXXXXXXXXX 14
DB 11248 RRRSSTASRTSR 11259
RESULT 9
AAB71432
ID AAB71432 standard; peptide; 15 AA.
XX
XX AAB71432;
AC
XX 27-NOV-2002 (first entry)
DT
DE Peptide Arg Helix #3 for construction of Tris-Arg helix #3.
XX
KW Sepsis; branched chain peptide; antibacterial; immunosuppressive;
KW endotoxin; helix peptide.
XX
XX Synthetic.
OS
XX Key Location/Qualifiers
FH
FT Modified-site 1
FT /note= "This residue has a side chain C(O)-NepsilonH-
FT (CH2)3-Tris-ArgHel#3, where the Tris-ArgHel#3 is
FT represented in AAB71431"
FT Modified-site 16
FT /note= "Acylated residue"
FT
XX

PN EP1232754-A2.
XX
PD 21-AUG-2002.
XX
XX 14-FEB-2002; 2002EP-00251027.
PF
XX 14-FEB-2001; 2001US-0268410P.
XX
XX (COMM-) COMMONWEALTH BIOTECHNOLOGIES INC.
PA
XX Harris RB, Wolz RL, Wolz G;
XX WPI; 2002-659478/71.
PI
DR
XX Use of cationic helix peptides for treatment of sepsis and for the
PT detection and removal of endotoxins.
PT
XX Disclosure; Fig 2; 18pp; English.
PS
XX This invention describes a novel use of antibacterial and
CC immunosuppressive peptides designated Arg Helix 2, Bis Arg Helix 2, Tetra
CC -Arg Helix 2 or Tris-Arg Helix 3 for the manufacture of a medicament for
CC the treatment of sepsis and the detection and removal of endotoxins. The
CC peptides of the invention are used in a method for detecting endotoxin in
CC a sample comprising contacting the sample with a labelled helix peptide
CC and then detecting the presence of any labelled molecule bound to
CC endotoxin. The peptides can also be used in a method for removing
CC endotoxin in a sample which comprises exposing the sample to a helix
CC peptide, bound to a solid support, then collecting the sample. The
CC endotoxin removal may be in vivo, or the peptides may be used to form an
CC affinity trap for endotoxins in e.g. dialysis-type treatments, or for
CC removal of endotoxins from plasma fractionation products. They are also
CC used as model frameworks for endotoxin binding from which new analogues
CC may be designed. This sequence represents the peptide Arg Helix #3 which
CC is used in the construction of the branched chain peptide Tris-Arg Helix
CC #3 described in the method of the invention
XX
SQ Sequence 15 AA;
Query Match 90.0%; Score 18; DB 5; Length 15;
Best Local Similarity 33.3%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 3 RXXXXXXXXX 14
DB 1 RRAAARAAARRAR 12
RESULT 10
AAB71430
ID AAB71430 standard; peptide; 16 AA.
XX
XX AAB71430;
AC
XX 27-NOV-2002 (first entry)
DT
XX Peptide Tris-Arg Helix #3 fragment.
DE
XX Sepsis; branched chain peptide; antibacterial; immunosuppressive;
KW endotoxin; helix peptide.
KW
XX Synthetic.
XX
XX Key Location/Qualifiers
FH
FT Modified-site 16
FT /note= "Ala is modified by unidentified R1 group"
XX
XX EP1232754-A2.
PN
XX 21-AUG-2002.
PD
XX 14-FEB-2002; 2002EP-00251027.
PF
XX

PR 14-FEB-2001; 2001US-0268410P.
XX (COMM-) COMMONWEALTH BIOTECHNOLOGIES INC.
XX
XX Harris RB, Wolz RL, Wolz G;
XX WPI; 2002-659478/71.
XX
XX Use of cationic helix peptides for treatment of sepsis and for the
PT detection and removal of endotoxins.
XX
XX Disclosure; Fig 1B; 18pp; English.
XX
XX This invention describes a novel use of antibacterial and
CC immunosuppressive peptides designated Arg Helix 2, Bis Arg Helix 2, Tetra
CC -Arg Helix 2 or Tris-Arg Helix 3 for the manufacture of a medicament for
CC the treatment of sepsis and the detection and removal of endotoxins. The
CC peptides of the invention are used in a method for detecting endotoxin in
CC a sample comprising contacting the sample with a labelled helix peptide
CC and then detecting the presence of any labelled molecule bound to
CC endotoxin. The peptides can also be used in a method for removing
CC endotoxin in a sample which comprises exposing the sample to a helix
CC peptide, bound to a solid support, then collecting the sample. The
CC endotoxin removal may be in vivo, or the peptides may be used to form an
CC affinity trap for endotoxins in e.g. dialysis-type treatments, or for
CC removal of endotoxins from plasma fractionation products. They are also
CC used as model frameworks for endotoxin binding from which new analogues
CC may be designed. This sequence represents the peptide Arg Helix #3 which
CC is used in the construction of Tris-Arg Helix #3, a branched chain
CC peptide described in the method of the invention
XX
XX Sequence 16 AA;
SQ

Query Match 90.0%; Score 18; DB 5; Length 16;
Best Local Similarity 33.3%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 3 RXXXXXXXXXR 14
Db 2 RRAAARARRAR 13

RESULT 11
AAY87840
ID AAY87840 standard; peptide; 19 AA.
XX
XX AAY87840;
XX
XX 01-SEP-2000 (first entry)
XX Heparin binding peptide Bis-Arg helix #2.
XX
XX Heparin binding peptide; antagonist; cardiovascular; coagulant;
KW bleeding wound; vascular anastomoses; leaking prosthetic vascular graft;
KW protamine substitute; treatment.
XX
XX Synthetic.
OS
XX
XX EP999219-A2.
XX
XX 10-MAY-2000.
XX
XX 01-OCT-1999; 99EP-00119514.
XX
XX 06-OCT-1998; 98US-00166930.
XX
XX (COMM-) COMMONWEALTH BIOTECHNOLOGIES INC.
XX
XX Harris RB, Sobel M;
XX
XX WPI; 2000-306006/27.
XX
XX New heparin binding molecules, useful for reducing heparin content in a

PT mammal by reducing the anticoagulant effects of heparin.
XX
XX Example 1; Fig 1a; 39pp; English.
XX
XX This invention describes novel heparin binding molecules (I). The
CC molecules (I) are useful as heparin antagonist drugs for cardiovascular
CC application and specifically neutralize heparin's conventional
CC anticoagulant properties. (I) are also useful for counteracting actions
CC of heparin locally e.g. in bleeding wounds, vascular anastomoses or
CC leaking prosthetic vascular grafts. (I) is also useful combined in a
CC pharmaceutical composition with insulin, as a substitute for protamine
CC for use in treating diabetics. The heparin binding molecules (I)
CC specifically neutralize heparin's conventional anticoagulant properties
CC without causing deleterious hemodynamic side-effects or exacerbation of
CC the proliferative vascular response to injury. (I) are short-duration,
CC intravenous drugs to be used in elective or emergency situations which
CC can safely and specifically neutralize heparin's proliferative response
CC to injury. This sequence represents a heparin-binding peptide described
CC in the method of the invention
XX
XX Sequence 19 AA;
SQ

Query Match 90.0%; Score 18; DB 3; Length 19;
Best Local Similarity 33.3%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 3 RXXXXXXXXXR 14
Db 5 RRAAARARRAR 16

RESULT 12
AAB71428
ID AAB71428 standard; peptide; 19 AA.
XX
XX AAB71428;
XX
XX 27-NOV-2002 (first entry)
XX
XX Peptide Bis-Arg Helix #2 fragment #1.
XX
XX Sepsis; branched chain peptide; antibacterial; immunosuppressive;
KW endotoxin; helix peptide.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 19
FT /note= "Ala is modified by unidentified R1 group"
XX
XX EP1232754-A2.
XX
XX 21-AUG-2002.
XX
XX 14-FEB-2002; 2002EP-00251027.
XX
XX 14-FEB-2001; 2001US-0268410P.
XX
XX (COMM-) COMMONWEALTH BIOTECHNOLOGIES INC.
XX
XX Harris RB, Wolz RL, Wolz G;
XX
XX WPI; 2002-659478/71.
XX
XX Use of cationic helix peptides for treatment of sepsis and for the
PT detection and removal of endotoxins.
XX
XX Disclosure; Fig 1A; 18pp; English.
XX
XX This invention describes a novel use of antibacterial and
CC immunosuppressive peptides designated Arg Helix 2, Bis Arg Helix 2, Tetra
CC -Arg Helix 2 or Tris-Arg Helix 3 for the manufacture of a medicament for
CC the treatment of sepsis and the detection and removal of endotoxins. The

CC peptides of the invention are used in a method for detecting endotoxin in
 CC a sample comprising contacting the sample with a labelled molecule bound to
 CC and then detecting the presence of any labelled molecule bound to
 CC endotoxin. The peptides can also be used in a method for removing
 CC endotoxin in a sample which comprises exposing the sample to a helix
 CC peptide, bound to a solid support, then collecting the sample. The
 CC endotoxin removal may be in vivo, or the peptides may be used to form an
 CC affinity trap for endotoxins in e.g. dialysis-type treatments, or for
 CC removal of endotoxins from plasma fractionation products. They are also
 CC used as model frameworks for endotoxin binding from which new analogues
 CC may be designed. This sequence represents the peptide Arg Helix #2 which
 CC is used in the construction of B1s-Arg Helix #2, a branched chain peptide
 CC described in the method of the invention

XX Sequence 19 AA;

Query Match 90.0%; Score 18; DB 5; Length 19;
 Best Local Similarity 33.3%; Pred. NO. 5.9e+02;
 Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXX 14

DB 5 RRAAARARRR 16

RESULT 13

ID ABP00279 standard; protein; 59 AA.

XX ABP00279;

DT 24-JUN-2002 (first entry)

DE Human ORFX protein sequence SEQ ID NO:540.

XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
 KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
 KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
 KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
 KW hypertension; hypothyroidism; cholesterol ester storage disease;
 KW immune deficiency; immune disorder; infectious disease;
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
 KW myasthenia gravis.

XX Homo sapiens.

XX WO200192523-A2.

XX 06-DEC-2001.

XX 29-MAY-2001; 2001WO-US010836.

XX 30-MAY-2000; 2000US-0206132P.

PR 29-AUG-2000; 2000US-0228716P.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach MD;

XX WPI; 2002-106308/14.

DR N-PSDB; ABN16031.

XX Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and autoimmune disorders.

PS Disclosure; SEQ ID NO 540; 1037pp; English.

XX The present invention describes substantially purified human proteins
 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
 CC in the specification). ABN15762 to ABN27252 encode the human ORFX
 CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
 CC treating or preventing a pathology associated with an ORFX-associated

CC disorder in humans, and in the manufacture of a medicament for treating a
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
 CC sequences can be used in gene therapy. ORFX sequences can be used in the
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
 CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
 CC storage disease, various immune deficiencies and disorders, rheumatoid
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
 CC useful for treating burns, incisions, ulcers for treating osteoporosis,
 CC bone degenerative disorders, or periodontal disease, and for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues and conditions resulting from
 CC systemic cytokine damage. N.B. The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 59 AA;

Query Match 90.0%; Score 18; DB 5; Length 59;

Best Local Similarity 33.3%; Pred. No. 1.4e+03;

Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXX 14

DB 43 RRSRTARASR 54

RESULT 14

ID ADX75905
 ID ADX75905 standard; protein; 64 AA.

XX AC ADX75905;

XX 21-APR-2005 (first entry)

XX Plant full length insert polypeptide seqid 45271.

XX plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content.

XX Unidentified.

XX US2004034888-A1.

XX 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

XX 06-MAY-1999; 99US-00304517.

PR 05-NOV-2001; 2001US-00985678.

XX (LIUJ/) LIU J.

PA (ZHOU/) ZHOU Y.

PA (KOVA/) KOVALIC D K.

PA (SCRE/) SCREEN S E.

PA (TAB/) TABASKA J E.

PA (CAOY/) CAO Y.

XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX WPI; 2004-180133/17.

XX New recombinant DNA construct, useful for improving plant tolerance to

PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.

XX Claim 1; SEQ ID NO 45271; 15pp; English.

PS The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. the polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.

XX SQ Sequence 64 AA;

Query Match 90.0%; Score 18; DB 8; Length 64;
 Best Local Similarity 33.3%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 3 RXXXXXXXXX 14
 |||||
 Db 19 RRTSSRRTRATR 30

RESULT 15

AAU41918
 ID AAU41918 standard; protein; 77 AA.

XX AAU41918;

DT 13-FEB-2002 (first entry)

XX Propionibacterium acnes immunogenic protein #2814.

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.

XX Propionibacterium acnes.

XX WO200181581-A2.

XX 01-NOV-2001.

XX 20-APR-2001; 2001WO-US012865.

XX 21-APR-2000; 2000US-0199047P.

PR 02-JUN-2000; 2000US-0208841P.

PR 07-JUL-2000; 2000US-0216747P.

XX (CORI-) CORIXA CORP.

XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX WPI; 2001-616774/71.

DR N-PSDB; AAS59515.

PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for

PT treating acne vulgaris.

XX Example 1; SEQ ID NO 3113; 1069pp; English.

CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 77 AA;

Query Match 90.0%; Score 18; DB 4; Length 77;
 Best Local Similarity 33.3%; Pred. No. 1.8e+03;
 Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 3 RXXXXXXXXX 14
 |||||
 Db 39 RRSMASTARSGR 50

Search completed: March 29, 2006, 01:44:11

Job time : 127.25 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 29, 2006, 01:44:43 ; Search time 20.5625 Seconds
(without alignments)
65.509 Million cell updates/sec

Title: US-10-712-447-210
Perfect score: 20
Sequence: 1 XXXRXXXXXXXRXR 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	90.0	79	S65036	nuclear basic prot
2	18	90.0	79	JH0404	basic nuclear prot
3	18	90.0	110	T30752	hypothetical prote
4	18	90.0	197	T18918	hypothetical prote
5	18	90.0	474	BVBRCE	cyab protein - Bor
6	18	90.0	574	T11162	hABC transport pro
7	18	90.0	660	D72453	hypothetical prote
8	18	90.0	668	A13144	two component sens
9	18	90.0	710	B98143	cv9Sy protein (AF0
10	17	85.0	195	G72697	hypothetical prote
11	17	85.0	207	D87267	hypothetical prote
12	17	85.0	238	A57198	splicing factor, a
13	17	85.0	241	G70705	hypothetical prote
14	17	85.0	310	T29423	probable transposa
15	17	85.0	317	PQ0339	hypothetical prote
16	17	85.0	344	S59043	spilling factor SR
17	17	85.0	395	E82796	hypothetical prote
18	17	85.0	436	T36706	hypothetical prote
19	17	85.0	461	A70837	probable proteinase
20	17	85.0	520	E87435	conserved hypothet
21	17	85.0	571	T40911	probable PHD-type
22	17	85.0	717	T15340	hypothetical prote
23	17	85.0	724	B85045	probable calcium c
24	17	85.0	1017	T31354	probable potassium
25	17	85.0	1577	T13722	hypothetical prote
26	17	85.0	1622	JE0378	DNA (cytosine-5)-
27	17	85.0	2351	G71415	hypothetical prote
28	17	85.0	3144	A46068	Huntington disease
29	16	80.0	52	FN0081	sperm chromatin pr

RESULT 1

S65036
nuclear basic protein SP4, sperm-specific - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S65036
R:Mita, K.; Ariyoshi, N.; Abe, S.; Takamune, K.; Katagiri, C.
Biochim. Biophys. Acta 1245, 430-438, 1995
A:Title: Structure of genes for sperm-specific nuclear basic protein (SP4) in Xenopus la
A:Reference number: S65036; MUID:96125743; PMID:8541323
A:Accession: S65036
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-79 <MIT>
A:Cross-references: UNIPARC:UPI000017BF96; EMBL:D45253
A:Note: the authors translated the codon TAT for residue 73 as Thr
C:Genetics:
A:Gene: XLSP41
A:Introns: 76/1

Query Match 90.0%; Score 18; DB 2; Length 79;
Best Local Similarity 33.3%; Pred. No. 46;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXRXR 14
DB 45 RRARTSTARRAR 56

RESULT 2

JH0404
basic nuclear protein SP4 precursor, sperm-specific - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: JH0404; PU0021; S65037; S65038; S65039
R:Hiyoshi, H.; Uno, S.; Yokota, T.; Katagiri, C.; Nishida, H.; Takai, M.; Agata, K.; Egu
Exp. Cell Res. 194, 95-99, 1991
A:Title: Isolation of cDNA for a Xenopus sperm-specific basic nuclear protein (SP4) and
A:Reference number: JH0404; MUID:91200205; PMID:2015853
A:Accession: JH0404
A:Molecule type: mRNA
A:Residues: 1-79 <HIY>
A:Cross-references: UNIPROT:P24056; UNIPARC:UPI000000D6D6; GB:D00916; NID:G2222970; PIDN
A:Experimental source: round spermatid
A:Accession: PU0021
A:Molecule type: protein
A:Residues: 2-11;12-43;65-74;75-79 <HI2>
A:Cross-references: UNIPARC:UPI000017BF78; UNIPARC:UPI000017BF79; UNIPARC:UPI000017BF7A;
R:Mita, K.; Ariyoshi, N.; Abe, S.; Takamune, K.; Katagiri, C.
Biochim. Biophys. Acta 1245, 430-438, 1995
A:Title: Structure of genes for sperm-specific nuclear basic protein (SP4) in Xenopus la
A:Reference number: S65036; MUID:96125743; PMID:8541323

30	16	80.0	57	2	E86930	hypothetical prote
31	16	80.0	61	2	S39425	protamine pl - duc
32	16	80.0	65	1	VHNVBM	nucleocapsid prote
33	16	80.0	79	2	A82875	ribosomal protein
34	16	80.0	88	2	AC2616	30S ribosomal prot
35	16	80.0	88	2	B97398	30S ribosomal prot
36	16	80.0	90	2	S29941	late embryogenesis
37	16	80.0	91	2	G87249	ribosomal protein
38	16	80.0	101	2	S21225	sperm protein EM6
39	16	80.0	125	2	F72785	hypothetical prote
40	16	80.0	126	2	D71162	hypothetical prote
41	16	80.0	139	2	C95386	protein [imported
42	16	80.0	142	2	B72683	hypothetical prote
43	16	80.0	144	2	T14796	hypothetical prote
44	16	80.0	175	2	A26882	plf2 hypothetical
45	16	80.0	184	2	G75510	hypothetical prote

[illegible]

A;Residues: 1-207 <STO>
A;Cross-references: UNIPROT:Q9ABS1; UNIPARC:UPI00000C6F4B; GB:AE005673; NID:g13421262; P
C;Genetics:
A;Gene: CC0149

Query Match 85.0%; Score 17; DB 2; Length 207;
Best Local Similarity 33.3%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXXR 14
|||
Db 2 RRSRSTRSRETR 13

RESULT 12
A57198
splicing factor, arginine/serine-rich 7 - human
N;Alternate names: splicing factor 9G8
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 31-Dec-2004
C;Accession: A57198; S46319
R;Popielarz, M.; Cavaloc, Y.; Mattei, M.G.; Gattoni, R.; Stevenin, J.
J. Biol. Chem. 270, 17830-17835, 1995
A;Title: The gene encoding human splicing factor 9G8. Structure, chromosomal localization
A;Reference number: A57198; MUID:95355374; PMID:7629084
A;Accession: A57198
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-238 <RES>
A;Cross-references: UNIPROT:Q16629; UNIPARC:UPI00000D853; GB:L41887; NID:g950423; PIDN:
R;Cavaloc, Y.; Popielarz, M.; Fuchs, J.P.; Gattoni, R.; Stevenin, J.
EMBO J. 13, 2639-2649, 1994
A;Title: Characterization and cloning of the human splicing factor 9G8: a novel 35 kDa f
A;Reference number: S46319; MUID:94283389; PMID:8013463
A;Accession: S46319
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-238 <CAV>
A;Cross-references: UNIPARC:UPI00000D853; EMBL:L22253; NID:g506401; PIDN:AAA35495.1; PI
C;Genetics:
A;Gene: GDB:SFRS7; 9G8
A;Cross-references: GDB:378350; OMIM:600572
A;Map position: 2p22-2p21
A;Introns: 10/1; 70/2; 129/2; 154/2; 191/2; 209/2; 221/2
F;12-74/Domain: ribonucleoprotein repeat homology <RRM3>

Query Match 85.0%; Score 17; DB 2; Length 238;
Best Local Similarity 33.3%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXXR 14
|||
Db 169 RRSASLRSSR 180

RESULT 13
G70705
hypothetical protein Rv0756c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: G70705
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: G70705
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-241 <COL>
A;Cross-references: UNIPROT:P71813; UNIPARC:UPI00000D46FB; GB:Z80226; GB:AL123456; NID:g

A;Experimental source: strain H37RV
C;Genetics:
A;Gene: Rv0756c

Query Match 85.0%; Score 17; DB 2; Length 241;
Best Local Similarity 33.3%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXXR 14
|||
Db 225 RRSRSRVSQR 236

RESULT 14
T29423
probable transposase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29423
R;Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1998
A;Reference number: Z20619
A;Accession: T29423
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-310 <PAR>
A;Cross-references: UNIPROT:O86606; UNIPARC:UPI00000DAD10; EMBL:AL031155; NID:el313489; I
C;Genetics:
A;Note: SC3A7.05c

Query Match 85.0%; Score 17; DB 2; Length 310;
Best Local Similarity 33.3%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXXR 14
|||
Db 262 RRRTPASARSAR 273

RESULT 15

PQ0339
hypothetical protein 317 - Lymantria dispar nuclear polyhedrosis virus (fragment)
N;Alternate names: ORFA protein
C;Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
C;Accession: PQ0339
R;Bjornson, R.M.; Rohrmann, G.F.
J. Gen. Virol. 73, 1499-1504, 1992
A;Title: Nucleotide sequence of the polyhedron envelope protein gene region of the Lymantria
A;Reference number: PQ0339; MUID:92300345; PMID:1607868
A;Accession: PQ0339
A;Molecule type: DNA
A;Residues: 1-317 <BJO>
A;Cross-references: UNIPARC:UPI000017A7C2; DBJ:D10836

Query Match 85.0%; Score 17; DB 2; Length 317;
Best Local Similarity 33.3%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXXR 14
|||
Db 9 RRADGASARRSR 20

Search completed: March 29, 2006, 01:50:04
Job time : 21.5625 secs

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OM protein - protein search, using sw model

Run on: March 29, 2006, 01:39:37 ; Search time 129.062 Seconds
(without alignments)
76.532 Million cell updates/sec

Title: US-10-712-447-210
Perfect score: 20
Sequence: 1 XRRXXXXXXXXX 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	414	Q4NWE6	anaeromyxob
2	20	100.0	452	Q7RWX1	neurospora
3	20	100.0	994	Q96SV1	caenorhabdi
4	20	100.0	1139	Q4SDD4	tetragoni
5	19	95.0	194	Q74EX0	geobacter s
6	19	95.0	214	Q7FOM2	oryza sativ
7	19	95.0	444	Q4LNR3	burkholderi
8	19	95.0	497	AMPA_SYNEL	86d146 synechococ
9	19	95.0	817	PERQ1_HUMAN	Q75420 homo sapien
10	19	95.0	833	Q4QE71	leishmania
11	19	95.0	856	Q4NSL6	9DELTA
12	18	90.0	57	Q5N831	oryza sativ
13	18	90.0	78	SP4_XENLA	Q53X49 xenopus lae
14	18	90.0	79	Q53X49	XENLA
15	18	90.0	85	Q6XN62	RHOER
16	18	90.0	102	Q6ZBE3	BURMA
17	18	90.0	109	Q11376	MCV1
18	18	90.0	110	Q98316	MCV1
19	18	90.0	112	Q52840	ORYSA
20	18	90.0	115	Q6TWS5	POXV
21	18	90.0	120	Q4NDP5	5MICC
22	18	90.0	133	Q69MP7	ORYSA
23	18	90.0	138	Q7X8A7	ORYSA
24	18	90.0	146	Q4N8B7	THEIPA
25	18	90.0	183	VC07	ADEB2
26	18	90.0	183	Q7M6E8	ADEB2
27	18	90.0	188	Q5ZD02	ORYSA
28	18	90.0	190	Q8LMA3	ORYSA
29	18	90.0	190	Q62AV1	BURMA
30	18	90.0	193	Q7G4Q0	ORYSA
31	18	90.0	197	Q17626	CAEEL

32	18	90.0	197	2	Q7EYP7	ORYSA
33	18	90.0	210	2	Q8LHV7	ORYSA
34	18	90.0	210	2	Q63X19	BURPFA
35	18	90.0	216	2	Q5YSD5	NOCPA
36	18	90.0	226	2	Q828F2	STRAW
37	18	90.0	313	2	Q5B410	EMENI
38	18	90.0	344	2	Q9RJR6	STRCO
39	18	90.0	348	2	Q6EQ52	ORYSA
40	18	90.0	352	2	Q5W6D5	ORYSA
41	18	90.0	392	2	Q4NTZ2	9DELTA
42	18	90.0	447	2	Q4LPK5	9BURK
43	18	90.0	462	2	Q4IQ72	GIBZE
44	18	90.0	474	1	CYAE	BORPE
45	18	90.0	474	2	Q7WLM9	BORPE

ALIGNMENTS

RESULT 1
Q4NWE6_9DELTA PRELIMINARY; PRT; 414 AA.
AC Q4NWE6;
DT 13-SEP-2005 (Tremblrel. 31, Created)
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
DE 13-SEP-2005 (Tremblrel. 31, Last annotation update)
DE ATP-binding region, ATPase-like:Histidine Kinase A, N-terminal precursor.
DE ORFNames=AdehDRAFT_3131;
OS Anaeromyxobacter dehalogenans 2CP-C.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
OX NCBI_TaxID=290397;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.;
RA "Sequencing of the draft genome assembly of Anaeromyxobacter dehalogenans 2CP-C";
RT dehalogenans 2CP-C";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Anaeromyxobacter dehalogenans 2CP-C";
RT dehalogenans 2CP-C";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
CC EMBL; AAHD01000008; EAL79882.1; -; Genomic_DNA.
KW ATP-binding; Kinase; Signal.
FT SIGNAL 1 32
SQ SEQUENCE 414 AA; 41594 MW; 0ADF0F0DCA0B0C53 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 414;
Best Local Similarity 33.3%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXX 14
DB 189 RRSAAAAAAR 200

RESULT 2
Q7RWX1_NEUCR PRELIMINARY; PRT; 452 AA.
ID Q7RWX1;
AC Q7RWX1;
DT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)

```

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU08793.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rahman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi B.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kanveysellis M., Mauceli E., Bielek C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Sella S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbels D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000758; EAA27000.1; -; Genomic DNA.
SQ SEQUENCE 452 AA; 47319 MW; F1737BB5A311FC3 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 452;
Best Local Similarity 33.3%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXRXR 14
DB 347 RRSSTTTTTRAR 358

RESULT 3
ID Q96SV1_CABEL PRELIMINARY; PRT; 994 AA.
AC Q96SV1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein Y48G1B.5.
GN ORFNames=Y48G1B.5;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol NZ;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; AC024794; AAK68497.1; -; Genomic DNA.
DR Ensembl; Y48G1B.5; Caenorhabditis elegans.
DR WormBase; WBGene00021670; Y48G1B.5.
DR WormPep; Y48G1B.5; CE26117.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 994 AA; 111289 MW; 73F6FC32D71D5CCC CRC64;

Query Match 100.0%; Score 20; DB 2; Length 994;
Best Local Similarity 33.3%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXRXR 14
DB 161 RRSSTTTTTSR 172

RESULT 5
ID Q74EX0_GEOSL PRELIMINARY; PRT; 194 AA.
AC Q74EX0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=GSU0839;
OS Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.
OX NCBI_TaxID=35554;
RN [1]
RP NUCLEOTIDE SEQUENCE.

Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXRXR 14
DB 595 RRATSTTTTTSR 606

RESULT 4
ID Q4SDD4_TETNG PRELIMINARY; PRT; 1139 AA.
AC Q4SDD4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 3 SCAP14639, whole genome shotgun sequence.
GN ORFNames=GSTENG00020093001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasiva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE01014639; CAG01348.1; -; Genomic DNA.
SQ SEQUENCE 1139 AA; 121432 MW; 7E2BD59621B51FCC CRC64;

Query Match 100.0%; Score 20; DB 2; Length 1139;
Best Local Similarity 33.3%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXRXR 14
DB 161 RRSSTTTTTSR 172

RESULT 5
ID Q74EX0_GEOSL PRELIMINARY; PRT; 194 AA.
AC Q74EX0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=GSU0839;
OS Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.
OX NCBI_TaxID=35554;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RC STRAIN=PCA / ATCC 51573;
RX PubMed=14671304; DOI=10.1126/science.1088727;
RA Meche B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA Davidesen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R.,
RA "Aken S.E., Lovley D.R., Fraser C.M.;
RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
RT environments.";
RL Science 302:1967-1969(2003).
DR EMBL; AE017180; AAR34169.1; -; Genomic_DNA.
DR TIGR; GSU0839; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 194 AA; 21055 MW; D0B0D918D3F2CACB CRC64;

Query Match 95.0%; Score 19; DB 2; Length 194;
Best Local Similarity 33.3%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXX 14
DB 139 RRSSSSLRTR 150

RESULT 6
ID Q7F0M2 Oryza PRELIMINARY; PRT; 214 AA.
AC Q7F0M2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein P0450A04.111.
GN Name=P0450A04.111;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
RT clone:P0450A04.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP004274; BAC83398.1; -; Genomic_DNA.
DR Gramene; Q7F0M2; -.
KW Hypothetical protein.
SQ SEQUENCE 214 AA; 23349 MW; E106D482D50E50C0 CRC64;

Query Match 95.0%; Score 19; DB 2; Length 214;
Best Local Similarity 33.3%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXX 14
DB 16 RRSSSSSRRSR 27

RESULT 7
ID Q4LNR3_9BURK PRELIMINARY; PRT; 444 AA.
AC Q4LNR3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Delta 1-pyrroline-5-carboxylate reductase (EC 1.5.1.2).
DR ORFNames=Bcen2424DRAFT_2557;
OS Burkholderia cenocepacia H12424.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=331272;
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RNA NUCLEOTIDE SEQUENCE.
RC STRAIN=H12424;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT H12424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H12424;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT H12424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHL01000036; EAM17718.1; -; Genomic_DNA.
KW Oxidoreductase.
SQ SEQUENCE 444 AA; 47128 MW; 6219556CF63899C7 CRC64;

Query Match 95.0%; Score 19; DB 2; Length 444;
Best Local Similarity 33.3%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXX 14
DB 96 RRATRAASRTAR 107

RESULT 8
ID AMPA_SYNEL STANDARD; PRT; 497 AA.
AC Q8DI46;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase)
DE (LAP) (Leucyl aminopeptidase).
GN Name=pepa; OrderedLocustNames=tlr1745;
OS Synecococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxID=32046;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=BP-1;
RX MEDLINE=2225144; PubMed=12240834;
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
RA Shampo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the thermophilic cyanobacterium
RT Thermosynechococcus elongatus BP-1.";
RL DNA Res. 9:123-130(2002).
CC -! FUNCTION: Presumably involved in the processing and regular
CC turnover of intracellular proteins. Catalyzes the removal of
CC unsubstituted N-terminal amino acids from various peptides (By
CC similarity).
CC -! CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-|-
CC Yaa-, in which Xaa is preferably Leu, but may be other amino acids
CC including Pro although not Arg or Lys, and Yaa may be Pro. Amino
CC acid amides and methyl esters are also readily hydrolyzed, but
CC rates on arylamides are exceedingly low.
CC -! COFACTOR: Binds 2 manganese ions per subunit (By similarity).
CC -! SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -! SIMILARITY: Belongs to the peptidase M17 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Anaeromyxobacter
RT dehalogenans 2CP-C.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHD01000021; EAL78630.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 856 AA; 89899 MW; F33C3D7D3B663665 CRC64;

Query Match 95.0%; Score 19; DB 2; Length 856;
Best Local Similarity 33.3%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
Db 738 RRSAAASRRR 749

RESULT 12
Q5N831_ORYSA PRELIMINARY; PRT; 57 AA.
AC Q5N831;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein B1099D03.55.
GN Name=B1099D03.55;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikono M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa M., Katagiri S., Kikuta A., Kobayashi T., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shinokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshinara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AP003431; BAD82385.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 57 AA; 65887 MW; 7A9814F81F280924 CRC64;

Query Match 90.0%; Score 18; DB 2; Length 57;
Best Local Similarity 33.3%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
Db 40 RRTDSALARSAR 51

RESULT 13
SP4_XENLA
ID SP4_XENLA PRT; 78 AA.
AC P24056;

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DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Sperm-specific basic nuclear protein SP4.
GN Name=SP4;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 1-43 AND 64-78.
RC TISSUE=Round spermatid;
RX MEDLINE=91200205; PubMed=2015853;
RA Hiyoishi H., Uno S., Yokota T., Katagiri C., Nishida H., Takai M.,
RA Agata K., Eguchi G., Abe S.-I.;
RT "Isolation of cDNA for a Xenopus sperm-specific basic nuclear protein
RT (SP4) and evidence for expression of SP4 mRNA in primary
RT spermatocytes.";
RL Exp. Cell Res. 194:95-99(1991).
CC -!- DEVELOPMENTAL STAGE: SP4 gene is transcribed in or before primary
CC spermatocyte stage but is translated at the round spermatid stage.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; D00916; BAA00762.1; -; mRNA.
DR PIR; JH0404; JH0404.
KW Direct protein sequencing; Nuclear protein; Repeat; Sperm.
FT INIT_MET 0
FT REPEAT 44 51
FT REPEAT 52 59
FT REPEAT 78 AA; 9194 MW; B342CD9CB8FD2FBA CRC64;
SQ SEQUENCE 78 AA; 9194 MW; B342CD9CB8FD2FBA CRC64;

Query Match 90.0%; Score 18; DB 1; Length 78;
Best Local Similarity 33.3%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
Db 44 RRARTSTARRAR 55

RESULT 14
Q53X49_XENLA PRELIMINARY; PRT; 79 AA.
ID Q53X49_XENLA PRELIMINARY;
AC Q53X49;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Sperm-specific nuclear basic protein (SP4).
GN Name=XLSP43; Synonyms=XLSP42, XLSP44;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=J;
RX MEDLINE=96125743; PubMed=8541323; DOI=10.1016/0304-4165(95)00124-7;
RT Mita K., Ariyoshi N., Abe S., Takamune K., Katagiri C.;
RT "Structure of genes for sperm-specific nuclear basic protein (SP4) in
RT Xenopus laevis.";
RL Biochim. Biophys. Acta 1245:430-438(1995).
DR EMBL; D45253; BAA08210.1; -; Genomic_DNA.
DR EMBL; D45253; BAA08211.1; -; Genomic_DNA.
DR EMBL; D45253; BAA08209.1; -; Genomic_DNA.
SQ SEQUENCE 79 AA; 9325 MW; 920C021D88FD70DC CRC64;

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Query Match 90.0%; Score 18; DB 2; Length 79;
Best Local Similarity 33.3%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
Db 45 RRARTSTARRAR 56

RESULT 15

Q6XN62 RHOER
ID Q6XN62 RHOER PRELIMINARY; PRT; 85 AA.
AC Q6XN62;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
DE ORFNames=PBD2.084;
GN Rhodococcus erythropolis.
OS Plasmid pBD2.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxID=1833;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BD2;
RX MEDLINE=22803265; PubMed=12923100;
RX DOI=10.1128/JB.185.17.5269-5274.2003;
RA Stecker C., Johann A., Herzberg C., Averhoff B., Gottschalk G.;
RT "Complete nucleotide sequence and genetic organization of the 210-
RT kilobase linear plasmid of Rhodococcus erythropolis BD2.";
RL J. Bacteriol. 185:5269-5274(2003).
DR EMBL; AY223810; AAP73969.1; -; Genomic_DNA.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 85 AA; 9111 MW; BE17D81E56DD0A2A CRC64;

Query Match 90.0%; Score 18; DB 2; Length 85;
Best Local Similarity 33.3%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
Db 14 RRTTTSVRAVR 25

Search completed: March 29, 2006, 01:49:13
Job time : 131.062 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 29, 2006, 01:49:32 ; Search time 29.3125 Seconds
(without alignments)
39.487 Million cell updates/sec

Title: US-10-712-447-210

Perfect score: 20

Sequence: 1 XRRXXXXXXXRXR 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCUTUS_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	95.0	133	2	US-09-252-991A-21845
2	19	95.0	189	2	US-09-252-991A-32376
3	19	95.0	442	2	US-09-252-991A-23285
4	18	90.0	16	1	US-08-660-592-11
5	18	90.0	16	2	US-09-166-930A-8
6	18	90.0	16	2	US-09-905-691-4
7	18	90.0	16	2	US-09-905-691-5
8	18	90.0	19	1	US-08-660-592-10
9	18	90.0	19	2	US-09-905-691-2
10	18	90.0	103	2	US-09-252-991A-32536
11	18	90.0	113	2	US-09-252-991A-17175
12	18	90.0	134	2	US-09-252-991A-21251
13	18	90.0	139	2	US-09-252-991A-24681
14	18	90.0	139	2	US-09-252-991A-26906
15	18	90.0	141	2	US-09-252-991A-23676
16	18	90.0	142	2	US-09-252-991A-31446
17	18	90.0	152	2	US-09-252-991A-25319
18	18	90.0	207	2	US-09-252-991A-21774
19	18	90.0	208	2	US-09-252-991A-17638
20	18	90.0	209	2	US-09-252-991A-21363
21	18	90.0	231	2	US-09-252-991A-17218
22	18	90.0	237	2	US-09-252-991A-32341
23	18	90.0	263	2	US-09-252-991A-19961
24	18	90.0	277	2	US-09-252-991A-28460
25	18	90.0	282	2	US-09-252-991A-29124
26	18	90.0	296	2	US-09-252-991A-20067
27	18	90.0	296	2	US-09-252-991A-32162

28	18	90.0	299	2	US-09-252-991A-21789	Sequence 21789, A
29	18	90.0	302	2	US-09-252-991A-18191	Sequence 18191, A
30	18	90.0	311	2	US-09-489-039A-9786	Sequence 9786, Ap
31	18	90.0	312	2	US-09-489-039A-14078	Sequence 14078, A
32	18	90.0	339	2	US-09-252-991A-22531	Sequence 22531, A
33	18	90.0	359	2	US-09-252-991A-29838	Sequence 29838, A
34	18	90.0	458	2	US-09-252-991A-18922	Sequence 18922, A
35	18	90.0	474	2	US-09-252-991A-17459	Sequence 17459, A
36	18	90.0	541	2	US-09-252-991A-33120	Sequence 33120, A
37	17	85.0	38	1	US-08-436-703B-17	Sequence 17, Appl
38	17	85.0	39	1	US-08-436-703B-5	Sequence 5, Appl
39	17	85.0	45	2	US-09-018-635-37	Sequence 37, Appl
40	17	85.0	45	2	US-09-912-962-37	Sequence 37, Appl
41	17	85.0	136	2	US-09-252-991A-20192	Sequence 20192, A
42	17	85.0	136	2	US-09-252-991A-30637	Sequence 30637, A
43	17	85.0	144	2	US-09-252-991A-17219	Sequence 17219, A
44	17	85.0	146	2	US-09-252-991A-20603	Sequence 20603, A
45	17	85.0	150	2	US-09-252-991A-24700	Sequence 24700, A

ALIGNMENTS

RESULT 1
US-09-252-991A-21845
; Sequence 21845, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21845
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21845

Query Match 95.0%; Score 19; DB 2; Length 133;
Best Local Similarity 33.3%; Pred No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RRRXXXXXXXRXR 14
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Db 22 RRSARTSTRATR 33

RESULT 2
US-09-252-991A-32376
; Sequence 32376, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32376
; LENGTH: 189
; TYPE: PRT

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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32376

Query Match          95.0%; Score 19; DB 2; Length 189;
Best Local Similarity 33.3%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXR 14
Db 34 RRTSASARRASR 45

RESULT 3
US-09-252-991A-23285
; Sequence 23285, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23285
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23285

Query Match          95.0%; Score 19; DB 2; Length 442;
Best Local Similarity 33.3%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXR 14
Db 307 RRAASRSRRTAR 318

RESULT 4
US-08-660-592-11
; Sequence 11, Application US/08660592
; Patent No. 5877153
; GENERAL INFORMATION:
; APPLICANT: HARRIS, Robert B.
; APPLICANT: SOBEL, Michael
; TITLE OF INVENTION: NOVEL HEPARIN BINDING PEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,592
; FILING DATE: 11-JUN-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 006338-001
; TELECOMMUNICATION INFORMATION:
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; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-660-592-11

Query Match          90.0%; Score 18; DB 1; Length 16;
Best Local Similarity 33.3%; Pred. NO. 1.1e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXR 14
Db 2 RRAAARAARRAR 13

RESULT 5
US-09-166-930A-8
; Sequence 8, Application US/09166930A
; Patent No. 6200955
; GENERAL INFORMATION:
; APPLICANT: HARRIS, Robert B.
; APPLICANT: SOBEL, Michael
; TITLE OF INVENTION: NOVEL HEPARIN BINDING PEPTIDES
; FILE REFERENCE: 006338-006
; CURRENT APPLICATION NUMBER: US/09/166,930A
; CURRENT FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: US 08/660,592
; PRIOR FILING DATE: 1996-06-11
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Tris Arg #3
US-09-166-930A-8

Query Match          90.0%; Score 18; DB 2; Length 16;
Best Local Similarity 33.3%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXR 14
Db 2 RRAAARAARRAR 13

RESULT 6
US-09-905-691-4
; Sequence 4, Application US/09905691
; Patent No. 6756206
; GENERAL INFORMATION:
; APPLICANT: Harris, Robert B.
; APPLICANT: Wolz, Russell L.
; APPLICANT: Wolz, Gabriella
; TITLE OF INVENTION: Adsorption and Removal of Endotoxin from Physiological
; FILE REFERENCE: 006338-017
; CURRENT APPLICATION NUMBER: US/09/905,691
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Tris-Arginine Helix #3
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US-09-905-691-4

Query Match 90.0%; Score 18; DB 2; Length 16;
Best Local Similarity 33.3%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXR 14
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Db 2 RRAAARARR 13

RESULT 7

US-09-905-691-5

; Sequence 5, Application US/09905691
; Patent No. 6756206
; GENERAL INFORMATION:
; APPLICANT: Harris, Robert B.
; APPLICANT: Wolz, Russell L.
; APPLICANT: Wolz, Gabriella
; TITLE OF INVENTION: Adsorption and Removal of Endotoxin from Physiological
; TITLE OF INVENTION: Fluids Using Cationic Helix Peptides
; FILE REFERENCE: 006338-017
; CURRENT APPLICATION NUMBER: US/09/905,691
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Tris-Arginine Helix #3
US-09-905-691-5

Query Match 90.0%; Score 18; DB 2; Length 16;
Best Local Similarity 33.3%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXR 14
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Db 2 RRAAARARR 13

RESULT 8

US-08-660-592-10

; Sequence 10, Application US/08660592
; Patent No. 6871153
; GENERAL INFORMATION:
; APPLICANT: HARRIS, Robert B.
; APPLICANT: SOBELL, Michael
; TITLE OF INVENTION: NOVEL HEPARIN BINDING PEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,592
; FILING DATE: 11-JUN-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 006338-001
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-660-592-10

Query Match 90.0%; Score 18; DB 1; Length 19;
Best Local Similarity 33.3%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXR 14
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Db 5 RRAAARARR 16

RESULT 9

US-09-905-691-2
; Sequence 2, Application US/09905691
; Patent No. 6756206
; GENERAL INFORMATION:
; APPLICANT: Harris, Robert B.
; APPLICANT: Wolz, Russell L.
; APPLICANT: Wolz, Gabriella
; TITLE OF INVENTION: Adsorption and Removal of Endotoxin from Physiological
; TITLE OF INVENTION: Fluids Using Cationic Helix Peptides
; FILE REFERENCE: 006338-017
; CURRENT APPLICATION NUMBER: US/09/905,691
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Bis-Arginine Helix #2
US-09-905-691-2

Query Match 90.0%; Score 18; DB 2; Length 19;
Best Local Similarity 33.3%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXR 14
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Db 5 RRAAARARR 16

RESULT 10

US-09-252-991A-32536
; Sequence 32536, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32536
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32536

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Query Match          90.0%; Score 18; DB 2; Length 103;
Best Local Similarity 33.3%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXR 14
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Db 56 RRPSSATARRSR 67

RESULT 11
US-09-252-991A-17175
; Sequence 17175, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17175
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17175

Query Match          90.0%; Score 18; DB 2; Length 113;
Best Local Similarity 33.3%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXR 14
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Db 84 RRSACASSRAGR 95

RESULT 12
US-09-252-991A-21251
; Sequence 21251, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21251
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21251

Query Match          90.0%; Score 18; DB 2; Length 134;
Best Local Similarity 33.3%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXR 14
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Db 107 RRAARSASRAGR 118

RESULT 13

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US-09-252-991A-24681
; Sequence 24681, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24681
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24681

Query Match          90.0%; Score 18; DB 2; Length 139;
Best Local Similarity 33.3%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db 16 RRSAGRRSR 27

RESULT 14
US-09-252-991A-26906
; Sequence 26906, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26906
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26906

Query Match          90.0%; Score 18; DB 2; Length 139;
Best Local Similarity 33.3%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXR 14
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Db 124 RRAARSARTAR 135

RESULT 15
US-09-252-991A-23676
; Sequence 23676, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788

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; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23676
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23676

Query Match      90.0%; Score 18; DB 2; Length 141;
Best Local Similarity 33.3%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy      3 RXXXXXXXXX 14
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Db      95 RRSADRSARSAR 106

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Job time : 30.3125 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2006, 02:05:02 ; Search time 119 Seconds
(without alignments)
49.156 Million cell updates/sec

Title: US-10-712-447-210
Perfect score: 20
Sequence: 1 XXXRXXXXXXRXR 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pcp.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	95.0	323	4	US-10-425-114-59856 Sequence 59856, A
2	19	95.0	533	4	US-10-085-198-124 Sequence 124, App
3	19	95.0	712	4	US-10-437-963-162715 Sequence 162715,
4	19	95.0	19725	4	US-10-084-846A-4 Sequence 4, Appli
5	18	90.0	16	3	US-09-905-691-4 Sequence 4, Appli
6	18	90.0	16	3	US-09-905-691-5 Sequence 5, Appli
7	18	90.0	19	3	US-09-905-691-2 Sequence 2, Appli
8	18	90.0	64	4	US-10-425-114-45271 Sequence 45271, A
9	18	90.0	87	4	US-10-437-963-184083 Sequence 184083,
10	18	90.0	118	4	US-10-425-115-325436 Sequence 325436,
11	18	90.0	120	4	US-10-437-963-104880 Sequence 104880,
12	18	90.0	124	4	US-10-425-115-286800 Sequence 286800,
13	18	90.0	127	3	US-09-764-847-886 Sequence 886, App
14	18	90.0	127	3	US-09-154-886 Sequence 118401,
15	18	90.0	137	4	US-10-437-963-118401 Sequence 118401,
16	18	90.0	136	4	US-10-425-114-50352 Sequence 50352, A
17	18	90.0	140	4	US-10-425-114-48089 Sequence 48089, A
18	18	90.0	140	4	US-10-437-963-113409 Sequence 113409,
19	18	90.0	149	4	US-10-437-963-156048 Sequence 156048,
20	18	90.0	173	4	US-10-437-963-197400 Sequence 197400,
21	18	90.0	190	4	US-10-425-114-56334 Sequence 56334, A
22	18	90.0	193	4	US-10-437-963-194450 Sequence 194450,
23	18	90.0	211	4	US-10-425-115-198672 Sequence 198672,
24	18	90.0	216	4	US-10-437-963-135886 Sequence 135886,
25	18	90.0	226	4	US-10-156-761-14245 Sequence 14245, A
26	18	90.0	245	3	US-09-738-626-3948 Sequence 3948, Ap
27	18	90.0	255	4	US-10-425-114-67642 Sequence 67642, A

28	18	90.0	255	4	US-10-437-963-194527 Sequence 194527,
29	18	90.0	272	4	US-10-437-963-150101 Sequence 150101,
30	18	90.0	281	4	US-10-425-114-46297 Sequence 46297, A
31	18	90.0	325	4	US-10-425-114-72973 Sequence 72973, A
32	18	90.0	357	4	US-10-282-122A-50703 Sequence 50703, A
33	18	90.0	403	4	US-10-437-963-168937 Sequence 168937,
34	18	90.0	497	4	US-10-437-963-125004 Sequence 125004,
35	18	90.0	19608	4	US-10-084-846A-8 Sequence 8, Appli
36	18	90.0	19695	4	US-10-084-846A-3 Sequence 3, Appli
37	17	85.0	36	4	US-10-050-704-210 Sequence 210, App
38	17	85.0	36	4	US-10-798-512-210 Sequence 55011, A
39	17	85.0	36	4	US-10-767-701-55011 Sequence 37, Appl
40	17	85.0	45	3	US-09-912-962-37 Sequence 32306, A
41	17	85.0	46	4	US-10-029-386-32306 Sequence 147658,
42	17	85.0	55	4	US-10-437-963-147658 Sequence 147658,
43	17	85.0	57	4	US-10-425-115-350524 Sequence 350524,
44	17	85.0	58	4	US-10-425-115-338158 Sequence 338158,
45	17	85.0	59	4	US-10-424-599-173763 Sequence 173763,

ALIGNMENTS

RESULT 1
US-10-425-114-59856
; Sequence 59856, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 59856
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3732-012-E4_FLI.pcp
US-10-425-114-59856

Query Match 95.0%; Score 19; DB 4; Length 323;
Best Local Similarity 33.3%; Pred. No. 2.2e+03;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXRXR 14
|||
DB 270 RRSAAASRTAR 281

RESULT 2
US-10-085-198-124
; Sequence 124, Application US/10085198
; Publication No. US20040009907A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-279
; CURRENT APPLICATION NUMBER: US/10/085,198
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/271,646
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/276,401
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,981
; PRIOR FILING DATE: 2001-08-13

; PRIOR APPLICATION NUMBER: 60/312,858
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/271,840
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/277,324
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/286,096
; PRIOR FILING DATE: 2001-04-21
; PRIOR APPLICATION NUMBER: 60/299,695
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/315,614
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/272,405
; PRIOR FILING DATE: 2001-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 653
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-085-198-124

Query Match 95.0%; Score 19; DB 4; Length 533;
Best Local Similarity 33.3%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
|||
Db 56 RRAAATRAAR 67

RESULT 3

US-10-437-963-162715
; Sequence 162715, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 162715
; LENGTH: 712
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_61780C.1.pep
US-10-437-963-162715

Query Match 95.0%; Score 19; DB 4; Length 712;
Best Local Similarity 33.3%; Pred. No. 4.2e+03;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
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Db 321 RRLASAAARAAR 332

RESULT 4

US-10-084-846A-4
; Sequence 4, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Robert B.
; APPLICANT: Wolz, Russell L.
; APPLICANT: Wolz, Gabriella
; TITLE OF INVENTION: Adsorption and Removal of Endotoxin from Physiological

; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREFZER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084,846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 19725
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 2: amino acid sequence encoded by coding strand 1.
; OTHER INFORMATION: Start codon: gat, Start position: nucleotide 2.
US-10-084-846A-4

Query Match 95.0%; Score 19; DB 4; Length 19725;
Best Local Similarity 33.3%; Pred. No. 6.1e+04;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
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Db 11142 RRRSTASRTSR 11153

RESULT 5

US-09-905-691-4
; Sequence 4, Application US/09905691
; Publication No. US20020164329A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Robert B.
; APPLICANT: Wolz, Russell L.
; APPLICANT: Wolz, Gabriella
; TITLE OF INVENTION: Adsorption and Removal of Endotoxin from Physiological
; TITLE OF INVENTION: Fluids Using Cationic Helix Peptides
; FILE REFERENCE: 006338-017
; CURRENT APPLICATION NUMBER: US/09/905,691
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Tris-Arginine Helix #3
US-09-905-691-4

Query Match 90.0%; Score 18; DB 3; Length 16;
Best Local Similarity 33.3%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
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Db 2 RRAAARAAR 13

RESULT 6

US-09-905-691-5
; Sequence 5, Application US/09905691
; Publication No. US20020164329A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Robert B.
; APPLICANT: Wolz, Russell L.
; APPLICANT: Wolz, Gabriella
; TITLE OF INVENTION: Adsorption and Removal of Endotoxin from Physiological

; TITLE OF INVENTION: Fluids Using Cationic Helix Peptides
; FILE REFERENCE: 006338-017
; CURRENT APPLICATION NUMBER: US/09/905,691
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Tris-Arginine Helix #3
US-09-905-691-5

Query Match 90.0%; Score 18; DB 3; Length 16;
Best Local Similarity 33.3%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXX 14
|||
DB 2 RRAAARAARR 13

RESULT 7
US-09-905-691-2
; Sequence 2, Application US/09905691
; Publication No. US20020164329A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Robert B.
; APPLICANT: Wolz, Russell L.
; APPLICANT: Wolz, Gabriella
; TITLE OF INVENTION: Adsorption and Removal of Endotoxin from Physiological
; TITLE OF INVENTION: Fluids Using Cationic Helix Peptides
; FILE REFERENCE: 006338-017
; CURRENT APPLICATION NUMBER: US/09/905,691
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Bis-Arginine Helix #2
US-09-905-691-2

Query Match 90.0%; Score 18; DB 3; Length 19;
Best Local Similarity 33.3%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXX 14
|||
DB 5 RRAAARAARR 16

RESULT 8
US-10-425-114-45271
; Sequence 45271, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 45271

; LENGTH: 64
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700431372_FLI.pep
US-10-425-114-45271

Query Match 90.0%; Score 18; DB 4; Length 64;
Best Local Similarity 33.3%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXX 14
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DB 19 RRTSSRTRATR 30

RESULT 9
US-10-437-963-184083
; Sequence 184083, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 184083
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_8110C.1.pep
US-10-437-963-184083

Query Match 90.0%; Score 18; DB 4; Length 87;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 RXXXXXXXXX 14
|||
DB 61 RRRSTRASRSR 72

RESULT 10
US-10-425-115-325436
; Sequence 325436, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 325436
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_59869C.1.pep

US-10-425-115-325436

Query Match 90.0%; Score 18; DB 4; Length 118;
Best Local Similarity 33.3%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXR 14
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Db 17 RRATAVSSRRTR 28

RESULT 11

US-10-437-963-104880
; Sequence 104880, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 104880
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(120)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_102172C.1.pep
US-10-437-963-104880

Query Match 90.0%; Score 18; DB 4; Length 120;
Best Local Similarity 33.3%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXR 14
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Db 56 RRSATAKQTR 67

RESULT 12

US-10-425-115-286800
; Sequence 286800, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 286800
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(124)

; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_24656C.1.pep
US-10-425-115-286800

Query Match 90.0%; Score 18; DB 4; Length 124;
Best Local Similarity 33.3%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXR 14
|||
Db 48 RRKAASRTSSR 59

RESULT 13

US-09-764-847-886
; Sequence 886, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 886
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (76)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (84)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (85)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (88)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (94)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (108)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (111)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-847-886

Query Match 90.0%; Score 18; DB 3; Length 127;
Best Local Similarity 33.3%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXXR 14
|||
Db 59 RRATSTARAIR 70

RESULT 14

US-10-092-154-886
; Sequence 886, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009C1
; CURRENT APPLICATION NUMBER: US/10/092,154

CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2003
Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 886
LENGTH: 127
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (76)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (84)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (85)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (88)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (94)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (108)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (111)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-092-154-886

Query Match 90.0%; Score 18; DB 4; Length 127;
Best Local Similarity 33.3%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 3 RXXXXXXXXR 14
Db 59 RRENTATRAIR 70

RESULT 15
US-10-437-963-118401
Sequence 118401, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 118401
LENGTH: 134
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(134)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_21716C.1.pap
US-10-437-963-118401

Query Match 90.0%; Score 18; DB 4; Length 134;

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Title: US-10-712-447-210
Perfect score: 20
Sequence: 1 XRRXXXXXXXRXR 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174695 seqs, 29494374 residues

Total number of hits satisfying chosen parameters: 174695

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /SIDSS/ptodata/1/pubpaa/US08 NEW PUB.pap:
2: /SIDSS/ptodata/1/pubpaa/US06 NEW PUB.pap:
3: /SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pap:
4: /SIDSS/ptodata/1/pubpaa/PCR_NEW PUB.pap:
5: /SIDSS/ptodata/1/pubpaa/US09 NEW PUB.pap:
6: /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pap:
7: /SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pap:
8: /SIDSS/ptodata/1/pubpaa/US60_NEW PUB.pap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	95.0	141	7	US-11-096-568A-4518
2	18	90.0	101	7	US-11-096-568A-25321
3	18	90.0	341	7	US-11-096-568A-27148
4	18	90.0	496	7	US-11-182-016-33
5	17	85.0	32	7	US-11-078-469-34
6	17	85.0	32	7	US-11-078-469-71
7	17	85.0	173	7	US-11-087-099-10728
8	17	85.0	189	7	US-11-096-568A-20087
9	17	85.0	192	7	US-11-096-568A-19930
10	17	85.0	200	7	US-11-096-568A-16604
11	17	85.0	211	7	US-11-087-099-6884
12	17	85.0	212	7	US-11-096-568A-20086
13	17	85.0	274	6	US-10-821-234-956
14	17	85.0	274	7	US-11-096-568A-22603
15	17	85.0	277	7	US-11-096-568A-19929
16	17	85.0	300	7	US-11-096-568A-27037
17	17	85.0	319	7	US-11-096-568A-24347
18	17	85.0	536	7	US-11-087-099-9046
19	17	85.0	2597	7	US-11-124-367A-466
20	17	85.0	2597	7	US-11-124-367A-468
21	17	85.0	3012	7	US-11-124-367A-465
22	17	85.0	3144	7	US-11-055-035-1
23	16	80.0	26	7	US-11-078-256-308
24	16	80.0	87	7	US-11-166-609-16
25	16	80.0	95	7	US-11-096-568A-25670

RESULT 1
US-11-096-568A-4518
; Sequence 4518, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 4518
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (1)..(141)
; OTHER INFORMATION: Ceres Seq. ID no. 13638657
US-11-096-568A-4518

Query Match 95.0%; Score 19; DB 7; Length 141;
Best Local Similarity 33.3%; Pred. No. 54;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RRRXXXXXXXRXR 14
Db 28 RRRSTTRRRR 39

RESULT 2
US-11-096-568A-25321
; Sequence 25321, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 25321
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:

Sequence 13882, A
Sequence 7047, Ap
Sequence 14539, A
Sequence 22510, A
Sequence 14218, A
Sequence 22509, A
Sequence 9617, Ap
Sequence 26671, A
Sequence 18247, A
Sequence 7046, Ap
Sequence 1290, Ap
Sequence 7045, Ap
Sequence 18246, A
Sequence 1876, Ap
Sequence 5420, Ap
Sequence 18556, A
Sequence 18555, A
Sequence 24229, A
Sequence 24216, A
Sequence 1598, Ap

; NAME/KEY: misc feature
; LOCATION: (1)..(101)
; OTHER INFORMATION: Ceres Seq. ID no. 13580080
US-11-096-568A-25321

Query Match 90.0%; Score 18; DB 7; Length 101;
Best Local Similarity 33.3%; Pred. No. 78;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
|||
Db 22 RRIATGAARSTR 33

RESULT 3

US-11-096-568A-27148
; Sequence 27148, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: Therby
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27148
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(341)
; OTHER INFORMATION: Ceres Seq. ID no. 15175533
US-11-096-568A-27148

Query Match 90.0%; Score 18; DB 7; Length 341;
Best Local Similarity 33.3%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
|||
Db 82 RRASSRRARASR 93

RESULT 4

US-11-182-016-33
; Sequence 33, Application US/11182016
; Publication No. US20060019294A1
; GENERAL INFORMATION:
; APPLICANT: SUGEN, INC.
; TITLE OF INVENTION: TYROSINE KINASE SUBSTRATE (TKS) PROTEINS
; FILE REFERENCE: 038602/0102
; CURRENT APPLICATION NUMBER: US/11/182,016
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US/09/958,359
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Tks 118
US-11-182-016-33

Query Match 90.0%; Score 18; DB 7; Length 496;
Best Local Similarity 33.3%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
|||

Db 273 RRAASRSRSRR 284

RESULT 5

US-11-078-469-34
; Sequence 34, Application US/11078469
; Publication No. US20050282755A1
; GENERAL INFORMATION:
; APPLICANT: HART, SCOTT A.
; APPLICANT: ZEH, KARIN
; APPLICANT: MACHLEIDT, THOMAS
; APPLICANT: STOLOV, DAVID
; APPLICANT: CONGER, DEE
; TITLE OF INVENTION: COMPOSITIONS HAVING ANTIMICROBIAL ACTIVITY AND USES
; FILE REFERENCE: ANS-2001-UT
; CURRENT APPLICATION NUMBER: US/11/078,469
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: 60/554,526
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: 60/618,948
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 34
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide moiety
; NAME/KEY: MOD_RES
; LOCATION: (1)_
; OTHER INFORMATION: H2N-Arg
US-11-078-469-34

Query Match 85.0%; Score 17; DB 7; Length 32;
Best Local Similarity 33.3%; Pred. No. 56;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
|||
Db 3 RRAATRVSRTRG 14

RESULT 6

US-11-078-469-71
; Sequence 71, Application US/11078469
; Publication No. US20050282755A1
; GENERAL INFORMATION:
; APPLICANT: HART, SCOTT A.
; APPLICANT: ZEH, KARIN
; APPLICANT: MACHLEIDT, THOMAS
; APPLICANT: STOLOV, DAVID
; APPLICANT: CONGER, DEE
; TITLE OF INVENTION: COMPOSITIONS HAVING ANTIMICROBIAL ACTIVITY AND USES
; FILE REFERENCE: ANS-2001-UT
; CURRENT APPLICATION NUMBER: US/11/078,469
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: 60/554,526
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: 60/618,948
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 71
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: peptide moiety
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)_RES
; OTHER INFORMATION: H2N-Arg
US-11-078-469-71

Query Match 85.0%; Score 17; DB 7; Length 32;
Best Local Similarity 33.3%; Pred. No. 56;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RRXXXXXXRXR 14
|||
Db 3 RRAATRVARTGR 14

RESULT 7
US-11-087-099-10728
; Sequence 10728, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 10728
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(173)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-087-099-10728

Query Match 85.0%; Score 17; DB 7; Length 173;
Best Local Similarity 33.3%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RRXXXXXXRXR 14
|||
Db 15 RRAATSRRAAR 26

RESULT 8
US-11-096-568A-20087
; Sequence 20087, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20087
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(189)
; OTHER INFORMATION: Ceres Seq. ID no. 12376847
US-11-096-568A-20087

Query Match 85.0%; Score 17; DB 7; Length 189;
Best Local Similarity 33.3%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RRXXXXXXRXR 14

Db 147 RRSARKTRRSAR 158
|||

RESULT 9
US-11-096-568A-19930
; Sequence 19930, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 19930
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(192)
; OTHER INFORMATION: Ceres Seq. ID no. 12375688
US-11-096-568A-19930

Query Match 85.0%; Score 17; DB 7; Length 192;
Best Local Similarity 33.3%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RRXXXXXXRXR 14
|||
Db 63 RRAAASGREER 74

RESULT 10
US-11-096-568A-16604
; Sequence 16604, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 16604
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(200)
; OTHER INFORMATION: Ceres Seq. ID no. 12353107
US-11-096-568A-16604

Query Match 85.0%; Score 17; DB 7; Length 200;
Best Local Similarity 33.3%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RRXXXXXXRXR 14
|||
Db 170 RRAAARGR 181

RESULT 11
US-11-087-099-6884
; Sequence 6884, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement

; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 6884
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Zea mays
US-11-087-099-6884

Query Match 85.0%; Score 17; DB 7; Length 211;
Best Local Similarity 33.3%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
|||
Db 178 RRAAKAARAR 189

RESULT 12
US-11-096-568A-20086
; Sequence 20086, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20086
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(212)
; OTHER INFORMATION: Ceres Seq. ID no. 12376846
US-11-096-568A-20086

Query Match 85.0%; Score 17; DB 7; Length 212;
Best Local Similarity 33.3%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
|||
Db 170 RRSARKTRRSAR 181

RESULT 13
US-10-821-234-956
; Sequence 956, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Grain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 956
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-956

Query Match 85.0%; Score 17; DB 6; Length 274;
Best Local Similarity 33.3%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
|||
Db 205 RRSRSASLRRSR 216

RESULT 14
US-11-096-568A-22603
; Sequence 22603, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22603
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(274)
; OTHER INFORMATION: Ceres Seq. ID no. 12409336
US-11-096-568A-22603

Query Match 85.0%; Score 17; DB 7; Length 274;
Best Local Similarity 33.3%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
|||
Db 217 RRSRAARRSR 228

RESULT 15
US-11-096-568A-19929
; Sequence 19929, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 19929
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(277)
; OTHER INFORMATION: Ceres Seq. ID no. 12375687
US-11-096-568A-19929

Query Match 85.0%; Score 17; DB 7; Length 277;
Best Local Similarity 33.3%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RXXXXXXXXX 14
|||
Db 148 RRAAASGREER 159

Search completed: March 29, 2006, 02:11:17
Job time : 14.125 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 29, 2006, 01:38:52 ; Search time 159.75 Seconds
(without alignments)
49.507 Million cell updates/sec

Title: US-10-712-447-5

Perfect score: 98

Sequence: 1 GIRRFLGSIWRFIRAFYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq 21:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	98	100.0	18	ADO34231	Ado34231 Synthetic
2	98	100.0	18	ADO34225	Ado34225 Synthetic
3	98	100.0	18	ADO34228	Ado34228 Synthetic
4	98	100.0	18	ADO34236	Ado34236 Synthetic
5	98	100.0	18	ADO34233	Ado34233 Synthetic
6	95	96.9	18	ADO34314	Ado34314 Synthetic
7	94	95.9	18	ADO34354	Ado34354 Synthetic
8	94	95.9	18	ADO34338	Ado34338 Synthetic
9	94	95.9	18	ADO34352	Ado34352 Synthetic
10	94	95.9	18	ADO34340	Ado34340 Synthetic
11	94	95.9	18	ADO34339	Ado34339 Synthetic
12	92	93.9	18	ADO34297	Ado34297 Synthetic
13	92	93.9	18	ADO34244	Ado34244 Synthetic
14	92	93.9	18	ADO34276	Ado34276 Synthetic
15	90	91.8	18	ADO34227	Ado34227 Synthetic
16	90	91.8	18	ADO34350	Ado34350 Synthetic
17	89	90.8	18	ADO34322	Ado34322 Synthetic
18	88	89.8	18	ADO34336	Ado34336 Synthetic
19	88	89.8	18	ADO34335	Ado34335 Synthetic
20	88	89.8	18	ADO34337	Ado34337 Synthetic
21	88	89.8	18	ADO34241	Ado34241 Synthetic
22	87	88.8	18	ADO34240	Ado34240 Synthetic
23	86	87.8	18	ADO34284	Ado34284 Synthetic
24	86	87.8	18	ADO34305	Ado34305 Synthetic

25	85	86.7	18	ADO34239	Ado34239 Synthetic
26	85	86.7	18	ADO34344	Ado34344 Synthetic
27	85	86.7	18	ADO34319	Ado34319 Synthetic
28	84	85.7	18	ADO34245	Ado34245 Synthetic
29	84	85.7	18	ADO34301	Ado34301 Synthetic
30	84	85.7	18	ADO34343	Ado34343 Synthetic
31	84	85.7	18	ADO34318	Ado34318 Synthetic
32	82	83.7	18	ADO34302	Ado34302 Synthetic
33	82	83.7	18	ADO34279	Ado34279 Synthetic
34	82	83.7	18	ADO34303	Ado34303 Synthetic
35	82	83.7	18	ADO34242	Ado34242 Synthetic
36	82	83.7	18	ADO34300	Ado34300 Synthetic
37	82	83.7	18	ADO34281	Ado34281 Synthetic
38	82	83.7	18	ADO34317	Ado34317 Synthetic
39	81	82.7	18	ADO34323	Ado34323 Synthetic
40	81	82.7	18	ADO34280	Ado34280 Synthetic
41	80	81.6	18	ADO34264	Ado34264 Synthetic
42	79	80.6	18	ADO34320	Ado34320 Synthetic
43	78	79.6	18	AA18917	AA18917 Lecithin:
44	78	79.6	18	AA19171	AA19171 Lecithin:
45	78	79.6	18	AA19425	AA19425 Lecithin:

ALIGNMENTS

RESULT 1

ADO34231

ID ADO34231 standard; peptide; 18 AA.

XX

AC ADO34231;

XX

DT 12-AUG-2004 (first entry)

XX

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 8.

XX

KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;

KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;

KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;

KW atherosclerosis; myocardial infarction; stroke; embolus; angina;

KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX

OS Synthetic.

XX

PN WO2004043403-A2.

XX

PD 27-MAY-2004.

XX

PF 13-NOV-2003; 2003WO-US036268.

XX

PA 13-NOV-2002; 2002US-0425821P.

XX

PI (UABR-) UAB RES FOUND.

XX

DR Anantharamiah GM, Garber DW, Datta G;

XX

WPI; 2004-411629/38.

XX

PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating

coronary artery disease, dysbetalipoproteinemia or atherosclerosis

comprises an amino acid sequence.

XX

PS Claim 4; SEQ ID NO 8; 79pp; English.

XX

CC The invention relates to a novel synthetic apolipoprotein-E mimicking

polypeptide. The invention further comprises an isolated nucleic acid

encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,

a host cell, a recombinant cell or a transgenic, non-human subject

(including animal or plant) comprising the synthetic apolipoprotein-E

mimicking polypeptide encoding polynucleotide; a composition comprising

the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and

an monoclonal antibody that specifically binds to the synthetic

apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

CC mimicking polypeptide has the following activities: antilipæmic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinæmia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;
 SQ Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18
 Db 1 GIRRFLGSIWRFIRAFYG 18
 |||||

RESULT 2
 ADO34225
 ID ADO34225 standard; peptide; 18 AA.

XX AC ADO34225;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking polypeptide related R19L peptide.

XX KW apolipoprotein-E mimicking polypeptide; antilipæmic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinæmia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 18 /note= "C-terminal amide"

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 2; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E

CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipæmic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinæmia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18
 Db 1 GIRRFLGSIWRFIRAFYG 18
 |||||

RESULT 3

ADO34228
 ID ADO34228 standard; peptide; 18 AA.

XX AC ADO34228;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 5.

XX KW apolipoprotein-E mimicking polypeptide; antilipæmic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinæmia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 5; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E

CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipemic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFYG 18
 |||||
 Db 1 GIRFLGSIWRFIRAFYG 18

RESULT 4
 ADO34236
 ID ADO34236 standard; peptide; 18 AA.

XX ADO34236;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 13.

KW apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 13; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising

CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipemic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFYG 18
 |||||
 Db 1 GIRFLGSIWRFIRAFYG 18

RESULT 5

ADO34233
 ID ADO34233 standard; peptide; 18 AA.

XX ADO34233;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 10.

KW apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 10; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and

CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFYG 18
 |||||
 Db 1 GIRFLGSIWRFIRAFYG 18
 |||||

RESULT 6
 ADO34314
 ID ADO34314 standard; peptide; 18 AA.
 AC ADO34314;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 91.
 XX
 KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
 XX
 OS Synthetic.
 XX
 PN WO2004043403-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 13-NOV-2003; 2003WO-US036268.
 XX
 PR 13-NOV-2002; 2002US-0425821P.
 XX
 PA (UABR-) UAB RES FOUND.
 XX
 PI Anantharamiah GM, Garber DW, Datta G;
 XX
 DR WPI; 2004-411629/38.
 XX
 PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.
 XX
 PS Claim 4; SEQ ID NO 91; 79pp; English.
 XX
 CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 SQ Sequence 18 AA;

Query Match 96.9%; Score 95; DB 8; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.8e-07;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFYG 18
 |||||
 Db 1 GIRFLGSIWRFIRAFYG 18
 |||||

RESULT 7
 ADO34354
 ID ADO34354 standard; peptide; 18 AA.
 AC ADO34354;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 131.
 XX
 KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
 XX
 OS Synthetic.
 XX
 PN WO2004043403-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 13-NOV-2003; 2003WO-US036268.
 XX
 PR 13-NOV-2002; 2002US-0425821P.
 XX
 PA (UABR-) UAB RES FOUND.
 XX
 PI Anantharamiah GM, Garber DW, Datta G;
 XX
 DR WPI; 2004-411629/38.
 XX
 PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.
 XX
 PS Claim 4; SEQ ID NO 131; 79pp; English.
 XX
 CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

CC mimicking polypeptide has the following activities: antilipemic, and
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.5e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRFLGSIWRFIRAFYG 18

Db 1 GLRRFLGSIWRFIRAFYG 18

RESULT 8

ADO34338

ID ADO34338 standard; peptide; 18 AA.

XX AC ADO34338;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 115.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.
 XX Claim 4; SEQ ID NO 115; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipemic,

CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.5e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRFLGSIWRFIRAFYG 18

Db 1 GLRRFLGSIWRFIRAFYG 18

RESULT 9

ADO34352

ID ADO34352 standard; peptide; 18 AA.

XX AC ADO34352;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 129.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.
 XX Claim 4; SEQ ID NO 129; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipemic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

CC antiangular. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.5e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRFLGSIWRFIRAFYG 18
 |||||:||||:||||
 Db 1 GIRFLGSIWRFIRAFYG 18

RESULT 10
 ADO34340
 ID ADO34340 standard; peptide; 18 AA.

XX
 AC ADO34340;

XX
 DT 12-AUG-2004 (first entry)

XX
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 117.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antiangular;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX
 OS Synthetic.

XX
 PN WO2004043403-A2.

XX
 PD 27-MAY-2004.

XX
 PF 13-NOV-2003; 2003WO-US036268.

XX
 PR 13-NOV-2002; 2002US-0425821P.

XX
 PA (UABR-) UAB RES FOUND.

XX
 PI Anantharamiah GM, Garber DW, Datta G;

XX
 DR WPI; 2004-411629/38.

XX
 PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX
 PS Claim 4; SEQ ID NO 117; 79pp; English.

XX
 CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antiangular. The synthetic apolipoprotein-E mimicking polypeptide is

CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.5e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRFLGSIWRFIRAFYG 18
 |||||:||||:||||
 Db 1 GIRFLGSIWRFIRAFYG 18

RESULT 11
 ADO34339

ID ADO34339 standard; peptide; 18 AA.

XX
 AC ADO34339;

XX
 DT 12-AUG-2004 (first entry)

XX
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 116.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antiangular;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX
 OS Synthetic.

XX
 PN WO2004043403-A2.

XX
 PD 27-MAY-2004.

XX
 PF 13-NOV-2003; 2003WO-US036268.

XX
 PR 13-NOV-2002; 2002US-0425821P.

XX
 PA (UABR-) UAB RES FOUND.

XX
 PI Anantharamiah GM, Garber DW, Datta G;

XX
 DR WPI; 2004-411629/38.

XX
 PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX
 PS Claim 4; SEQ ID NO 116; 79pp; English.

XX
 CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antiangular. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal

CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.5e-07;

Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18

Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 12

ADO34297

ID ADO34297 standard; peptide; 18 AA.

XX

AC ADO34297;

XX

DT 12-AUG-2004 (first entry)

XX

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 74.

XX

KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX

FN WO2004043403-A2.

XX

PD 27-MAY-2004.

XX

PF 13-NOV-2003; 2003WO-US036268.

XX

PR 13-NOV-2002; 2002US-0425821P.

XX

PA (UABR-) UAB RES FOUND.

XX

PI Anantharamiah GM, Garber DW, Datta G;

XX

DR WPI; 2004-411629/38.

XX

PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX

PS Claim 4; SEQ ID NO 74; 79pp; English.

XX

CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,

CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 93.9%; Score 92; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 5.1e-07;

Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18

Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 13

ADO34244

ID ADO34244 standard; peptide; 18 AA.

XX

AC ADO34244;

XX

DT 12-AUG-2004 (first entry)

XX

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 21.

XX

KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX

FN WO2004043403-A2.

XX

PD 27-MAY-2004.

XX

PF 13-NOV-2003; 2003WO-US036268.

XX

PR 13-NOV-2002; 2002US-0425821P.

XX

PA (UABR-) UAB RES FOUND.

XX

PI Anantharamiah GM, Garber DW, Datta G;

XX

DR WPI; 2004-411629/38.

XX

PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX

PS Claim 4; SEQ ID NO 21; 79pp; English.

XX

CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,

CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 93.9%; Score 92; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 5.1e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18
 |||||:|||||:|||||
 Db 1 GIRRFLGAIWRFIRSFYG 18

RESULT 14

ADO34276
 ID ADO34276 standard; peptide; 18 AA.

XX
 AC ADO34276;

XX
 DT 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 53.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
 XX Synthetic.

XX Key Location/Qualifiers
 FH Modified-site 1..18
 FT /note= "All Lys residues are DiMethyl-Lysine"

XX WO2004043403-A2.
 XX 27-MAY-2004.

XX
 XX 13-NOV-2003; 2003WO-US036268.
 XX 13-NOV-2002; 2002US-0425821P.

XX
 XX (UABR-) UAB RES FOUND.
 XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 53; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 93.9%; Score 92; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 5.1e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18
 |||||:|||||:|||||
 Db 1 GIKRFLGSIWRFIKAFYG 18

RESULT 15

ADO34227
 ID ADO34227 standard; peptide; 18 AA.

XX
 AC ADO34227;

XX
 DT 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking related R18L linear peptide.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
 XX Synthetic.

XX WO2004043403-A2.
 XX 27-MAY-2004.

XX
 XX 13-NOV-2003; 2003WO-US036268.
 XX 13-NOV-2002; 2002US-0425821P.

XX
 XX (UABR-) UAB RES FOUND.
 XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 4; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal

CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
CC chimpanzee or orangutan); for treating coronary artery disease,
CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
CC myocardial infarction or stroke; for breaking an embolus in the subject;
CC and also for treating angina. The synthetic apolipoprotein-E mimicking
CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
CC mimicking polypeptide of the invention.

XX
SQ Sequence 18 AA;

Query Match 91.8%; Score 90; DB 8; Length 18;
Best Local Similarity 94.4%; Pred. No. 1e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFVG 18
| | | | | | | | | | | | | | | |
Db 1 GIRFLGSIWRFIRAFVG 18

Search completed: March 29, 2006, 01:44:08
Job time : 159.75 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2006, 01:44:43 ; Search time 26.4375 Seconds
(without alignments)
65.509 Million cell updates/sec

Title: US-10-712-447-5

Perfect score: 98

Sequence: 1 GIRRFLGSIWRFIRAFYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	49.0	627	S76462	hypothetical prote
2	45	45.9	178	A75578	transcription regu
3	44	44.9	461	1 G64537	2-oxoglutarate/mal
4	44	44.9	589	2 A34341	poly(3-hydroxybuty
5	44	44.9	806	2 A84060	leucyl-tRNA synthe
6	44	44.9	861	2 H64102	leucine-tRNA ligas
7	43.5	44.4	1025	2 AH3568	acriflavin resista
8	43	43.9	265	2 T32316	hypothetical prote
9	43	43.9	489	2 B84733	probable cytochrom
10	43	43.9	516	2 T33269	hypothetical prote
11	43	43.9	812	2 A46417	NIPI protein - yea
12	43	43.9	1607	2 T04583	TMV resistance pro
13	42.5	43.4	407	2 T12085	reverse transcript
14	42.5	43.4	760	2 E84953	penicillin-binding
15	42	42.9	107	2 T52113	probable transcrip
16	42	42.9	214	2 T72540	hypothetical prote
17	42	42.9	228	2 T15530	hypothetical prote
18	42	42.9	237	2 B72692	hypothetical prote
19	42	42.9	246	2 I54412	MHC HLA-A cell sur
20	42	42.9	258	2 F71707	o-antigen export s
21	42	42.9	258	2 D97700	o-antigen export s
22	42	42.9	273	1 HLHU69	MHC class I histoc
23	42	42.9	365	1 HLHUA2	MHC class I histoc
24	42	42.9	365	2 I38443	gene HLA-A-0203 pr
25	42	42.9	365	2 I61902	MHC class I histoc
26	42	42.9	365	2 I37542	MHC class I histoc
27	42	42.9	365	2 I84448	MHC class I histoc
28	42	42.9	365	2 I61857	MHC HLA-A2.4a chai
29	42	42.9	365	2 I38442	gene HLA-A-0205 pr

ALIGNMENTS

RESULT 1

S76462

hypothetical protein - Synechocystis sp. (strain PCC 6803)

C:Species: Synechocystis sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C:Accession: S76462

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

S.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S76462

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-627 <KAN>

A:Cross-references: UNIPROT:P74489; UNIPARC:UPI00000C103F; EMBL:P90915; GB:AB001339; NID

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 49.0%; Score 48; DB 2; Length 627;

Best Local Similarity 38.9%; Pred. No. 8.1;

Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Oy 1 GIRRFLGSIWRFIRAFYG 18

Db 597 GLEQLGKIQWLQKFG 614

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Best Local Similarity 69.2%; Pred. No. 7.2;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IRREFLSIWRPFR 14
Db 23 ILRFLGGIWRLLNR 35

RESULT 3
G64537
2-oxoglutarate/malate translocator - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: G64537
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKernan,
J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.;
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: G64537
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-461 <TOM>
A;Cross-references: UNIPARC:UPI0000174217; GB:A6000511; TTGR:HP0143
C;Superfamily: 2-oxoglutarate/malate translocator

Query Match 44.9%; Score 44; DB 1; Length 461;
Best Local Similarity 53.8%; Pred. No. 26;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IRREFLSIWRPFR 14
Db 297 VRLLSWFWRPVR 309

RESULT 4
A34341
poly(3-hydroxybutyrate) synthase (EC 2.3.1.-) - Alcaligenes eutrophus
C;Species: Alcaligenes eutrophus
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C;Accession: A34341; A39190
R;Peoples, O.P.; Sinskey, A.J.
J. Biol. Chem. 264, 15298-15303, 1989
A;Title: Poly-beta-hydroxybutyrate (PHB) biosynthesis in Alcaligenes eutrophus H16. Ident
A;Reference number: A34341; MUID:89359357; PMID:2670936
A;Accession: A34341
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-589 <PEO>
A;Cross-references: UNIPROT:P23608; UNIPARC:UPI0000044953; GB:J05003; NID:g141958; PIDN:
A;Experimental source: strain H16
R;Schubert, P.; Krueger, N.; Steinbuechel, A.
J. Bacteriol. 173, 168-175, 1991
A;Title: Molecular analysis of the Alcaligenes eutrophus poly(3-hydroxybutyrate) biosynt
omoter.
A;Reference number: A39190; MUID:91100279; PMID:1987116
A;Accession: A39190
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-219 <SCH>
A;Cross-references: UNIPARC:UPI000016B162; GB:M64341; NID:g141964; PIDN:AAA21979.1; PID:
A;Note: the authors translated the codon TAC for residue 120 as Thr
C;Superfamily: poly(3-hydroxyalkanoic acid) synthase phbC
C;Keywords: acyltransferase

Query Match 44.9%; Score 44; DB 2; Length 589;
Best Local Similarity 47.6%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

Qy 3 RRFLGSIW-----RPTRAFY 17
||| | | | | | | | | |
```

```
Db 100 RRFAGDAWRNTLPYRFAAFY 120

RESULT 5
A84060
leucyl-tRNA synthetase leuS [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: A84060
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A84060
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-806 <STO>
A;Cross-references: UNIPROT:Q9K788; UNIPARC:UPI0000136555; GB:A6001518; GB:BA000004; NID:
A;Experimental source: strain C-125
C;Genetics:
A;Gene: leuS
C;Superfamily: leucine-tRNA ligase

Query Match 44.9%; Score 44; DB 2; Length 806;
Best Local Similarity 53.8%; Pred. No. 45;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GIRREFLSIWRFI 13
| | | | | : | | :
Db 622 GARRFLDRVWRLL 634

RESULT 6
H64102
leucine-tRNA ligase (EC 6.1.1.4) - Haemophilus influenzae (strain Rd KW20)
N;Alternate names: leucyl-tRNA synthetase
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: H64102
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: H64102
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-861 <TIGR>
A;Cross-references: UNIPROT:P43827; UNIPARC:UPI000013655F; GB:U32774; GB:L42023; NID:g15'
C;Genetics:
A;Gene: leuS
C;Superfamily: leucine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 44.9%; Score 44; DB 2; Length 861;
Best Local Similarity 46.2%; Pred. No. 48;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GIRREFLSIWRFI 13
| : | | | | : | :
Db 665 GAKRFLGRVWNLV 677

RESULT 7
AH3568
acriflavin resistance protein F [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AH3568
R;DelVecchio, V.G.; Kaputral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Ios, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
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Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
A;Reference number: AD3252; PMID:11756688
A;Accession: AH3568
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1025 <KUR>
A;Cross-references: UNIPROT:Q8YQ05; UNIPARC:UPI00000584C8; GB:AE008918; PIDN:AAL53715.1;
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BME110473
A;Map position: 11
C;Superfamily: hypothetical protein b2075

Query Match 44.4%; Score 43.5; DB 2; Length 1025;
Best Local Similarity 50.0%; Pred. No. 69;
Matches 8; Conservative 4; Mismatches 1; Indels 3; Gaps 1;

QY 5 FLGSWRFIRAFY 17
Db 531 FLGSVSWFMTLPRSPF 546

RESULT 8
T32316
hypothetical protein F31P4.4 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Dec-2004
C;Accession: T32316
R;Blanchard, M.; Kramer, J.; Elliott, G.; Twyman, B.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of *C. elegans* cosmid F31P4.
A;Reference number: Z21149
A;Accession: T32316
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-265 <BLA>
A;Cross-references: UNIPROT:O17136; UNIPARC:UPI000007D19A; EMBL:AF024503; PIDN:AAB70384.
A;Experimental source: strain Bristol N2; clone F31P4
C;Genetics:
A;Gene: CESP:F31P4.4
A;Map position: 5
A;Introns: 13/3; 67/2
C;Superfamily: *Caenorhabditis elegans* hypothetical protein T09F5.1

Query Match 43.9%; Score 43; DB 2; Length 265;
Best Local Similarity 53.8%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 LGSWRFIRAFY 18
Db 253 LASLWAFVHAFEG 265

RESULT 9
B84733
probable cytochrome P450 [imported] - *Arabidopsis thaliana*
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: B84733
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Niernan, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: B84733
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-489 <STO>
A;Cross-references: UNIPROT:Q9ZV72; UNIPARC:UPI000009D8ED; GB:AE002093; NID:G3831452; PI
C;Genetics:
A;Gene: At2g32440

A;Map position: 2
C;Superfamily: *Synechocystis* cytochrome P450 slr0574; cytochrome P450 homology

Query Match 43.9%; Score 43; DB 2; Length 489;
Best Local Similarity 54.5%; Pred. No. 40;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 LGSWRFIRAF 16
Db 54 IGNNWSEFLAP 64

RESULT 10

T33269
hypothetical protein C24B9.13 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33269
R;Murray, J.; Wohldmann, P.; Langston, Y.; O'Neal, D.
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of *C. elegans* cosmid C24B9.
A;Reference number: Z21310
A;Accession: T33269
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-516 <MUR>
A;Cross-references: UNIPROT:O76442; UNIPARC:UPI000007D477; EMBL:AF068709; PIDN:AAC19257.
A;Experimental source: strain Bristol N2; clone C24B9
C;Genetics:
A;Gene: CESP:C24B9.13
A;Map position: 5
A;Introns: 13/3; 67/2; 116/2; 268/2; 315/2; 364/2

Query Match 43.9%; Score 43; DB 2; Length 516;
Best Local Similarity 41.2%; Pred. No. 42;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 IRRELGSWRFIRAFY 18
Db 252 LKFFITSLWFMHAFDG 268

RESULT 11

A46417
NIP1 protein - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: nuclear import protein; protein YM9924.01c; protein YM9952.11c; prote
C;Species: *Saccharomyces cerevisiae*
C;Date: 21-Sep-1993 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A46417; S53979; S59302
R;Gu, Z.; Moerschell, R.P.; Sherman, F.; Goldfarb, D.S.
Proc. Natl. Acad. Sci. U.S.A. 89, 10355-10359, 1992
A;Title: NIP1, a gene required for nuclear transport in yeast.
A;Reference number: A46417; MUID:93066237; PMID:1332047
A;Accession: A46417
A;Molecule type: DNA
A;Residues: 1-812 <GUL>
A;Cross-references: UNIPROT:P32497; UNIPARC:UPI000017B2E1; EMBL:L02899
A;Note: sequence extracted from NCBI backbone (NCBIN:117849, NCBIP:117850)
R;Connor, R.; Churcher, C.M.
submitted to the EMBL Data Library, April 1995
A;Reference number: S53969
A;Accession: S53979
A;Molecule type: DNA
A;Residues: 571-582, 'Q', 584-640, 'K', 642, 'K', 644-812 <CON>
A;Cross-references: UNIPARC:UPI0000168ACD; EMBL:Z49212; NID:G798940; PID:G798951; MIPS:Y
R;Churcher, C.M.
submitted to the EMBL Data Library, September 1995
A;Reference number: S59302
A;Accession: S59302
A;Molecule type: DNA
A;Residues: 1-110, 'V', 112-582, 'Q', 584-602 <CHU>
A;Cross-references: UNIPARC:UPI0000168ACA; EMBL:Z54141; NID:G1072408; PID:G984682; MIPS
A;Experimental source: strain AB972


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GN Name=rzcb;
OS Rhizobium leguminosarum (biovar viciae).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_TaxID=387;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=305;
RX MEDLINE=21360352; PubMed=11467725; DOI=10.1139/cjm-47-6-495;
RA Venter A.P., Twelker S., Oresnik I.J., Hynes M.F.;
RT "Analysis of the genetic region encoding a novel rhizobiocin from
RT Rhizobium leguminosarum bv. viciae strain 305.";
RL Can. J. Microbiol. 47:495-502(2001).
DR EMBL; AF273216; AAC25076.1; -; Genomic_DNA.
DR HSP; P08716; IMT0.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005524; F: ATP binding; IEA.
DR GO; GO:0016887; F: ATPase activity; IEA.
DR GO; GO:0042626; F: ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0000156; F: nucleotide binding; IEA.
DR GO; GO:0008233; F: peptidase activity; IEA.
DR GO; GO:0008565; F: protein transporter activity; IEA.
DR GO; GO:0015031; P: protein transport; IEA.
DR GO; GO:0006508; P: proteolysis and peptidolysis; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011527; ABC_membrane_1.
DR InterPro; IPR001140; ABC_TM_transp.
DR InterPro; IPR003439; ABC_transp_like.
DR InterPro; IPR005074; Peptidase_C39.
DR InterPro; IPR010132; Type I_sec_HlyB.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR Pfam; PF03412; Peptidase_C39; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR TIGRFAMs; TIGR01846; type I sec HlyB; 1.
DR PROSITE; PS50929; ABC_TMIF; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
DR PROSITE; PS50990; PEPTIDASE_C39; 1.
SQ SEQUENCE 735 AA; 80717 MW; 0216259241F3630C CRC64;

Query Match 53.1%; Score 52; DB 2; Length 735;
Best Local Similarity 62.5%; Pred. No. 17;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFIRAF 16
|||:|||||
Db 161 GFRWFLPAIWRYRAF 176

RESULT 3
Q4LK44_9BURK PRELIMINARY; PRT; 408 AA.
AC Q4LK44;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Bcen2424DRAFT_1071;
OS Burkholderia cenocepacia H12424.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cenocepacia complex.
OX NCBI_TaxID=331272;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H12424;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT H12424.";
RT Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.

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RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H12424;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT H12424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -i- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHL0100063; EAM16412.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 408 AA; 45603 MW; 7F393888305911D2 CRC64;

Query Match 52.0%; Score 51; DB 2; Length 408;
Best Local Similarity 47.1%; Pred. No. 13;
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFIRAF 17
|||:|||||
Db 328 GIRQMLGHVWQWTRSS 344

RESULT 4
Q5GH72_HUMAN PRELIMINARY; PRT; 579 AA.
ID Q5GH72_HUMAN PRELIMINARY;
AC Q5GH72;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE XK-related protein 7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Huang C.-H., Chen Y.;
RT "A superfamily of XK-related genes (XRG) widely expressed in
RT vertebrates and invertebrates.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY534245; AAT07094.1; -; mRNA.
SQ SEQUENCE 579 AA; 63825 MW; D8D0FF64B9EDD53D CRC64;

Query Match 51.0%; Score 50; DB 2; Length 579;
Best Local Similarity 58.3%; Pred. No. 28;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 LGSIWRFIRAF 17
|||:|||||
Db 190 LGQVWRYLALY 201

RESULT 5
Q5GH56_RAT PRELIMINARY; PRT; 580 AA.
AC Q5GH56;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE XK-related protein 7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley;
RA Huang C.-H., Chen Y.;
RT "A superfamily of XK-related genes (XRG) widely expressed in

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RT vertebrates and invertebrates."
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY534261; AAT07110.1; -; mRNA.
SQ SEQUENCE 580 AA; 64337 MW; 8F4907F391B4F5BE CRC64;

Query Match 51.0%; Score 50; DB 2; Length 580;
Best Local Similarity 58.3%; Pred. No. 28;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 LGSIWRFIRAFY 17
Db 190 LGQVWRYLRALY 201

RESULT 6
Q5GH64 MOUSE PRELIMINARY; PRT; 580 AA.
ID Q5GH64;
AC Q5GH64;
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE XK-related protein 7.
GN Name=AY534253;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J;
RC Huang C.-H., Chen Y.;
RA "A superfamily of XK-related genes (XRG) widely expressed in
RT vertebrates and invertebrates."
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY534253; AAT07102.1; -; mRNA.
DR MGI: MGI:3526711; AY534253.
SQ SEQUENCE 580 AA; 64301 MW; F3291FABF4C5A826 CRC64;

Query Match 51.0%; Score 50; DB 2; Length 580;
Best Local Similarity 58.3%; Pred. No. 28;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 LGSIWRFIRAFY 17
Db 190 LGQVWRYLRALY 201

RESULT 7
Q84ZW1_PEA PRELIMINARY; PRT; 488 AA.
ID Q84ZW1_PEA;
AC Q84ZW1;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Ent-kaurenoic acid oxidase.
GN Name=KA01;
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Shoot;
RC MEDLINE=22417727; PubMed=12529541; DOI=10.1104/pp.012963;
RA Davidson S.E., Elliott R.C., Helliwell C.A., Poole A.T., Reid J.B.;
RT "The pea gene NA encodes ent-kaurenoic acid oxidase."
RL Plant Physiol. 131:335-344 (2003).
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum (By
CC similarity).
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL: AF537321; AAO23063.1; -; mRNA.
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DR GO: 0046872; P:metal ion binding; IEA.
DR GO: 0004497; F:monooxygenase activity; IEA.
DR GO: 0006118; P:electron transport; IEA.
DR InterPro: IPR001128; Cytochrome_P450.
DR InterPro: IPR002401; EP450I.
DR Pfam: PF00067; P450: 1.
DR PRINTS; PR00463; EP450I.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME P450; UNKNOWN 1.
KW Endoplasmic reticulum; Heme; Iron; Metal-binding; Monooxygenase;
KW Oxidoreductase.
SQ SEQUENCE 488 AA; 56478 MW; 503453CB6E43C830 CRC64;

Query Match 50.0%; Score 49; DB 2; Length 488;
Best Local Similarity 58.3%; Pred. No. 34;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 5 FLGSIWRFIRAF 16
Db 54 FIGNMSFLRAP 65

RESULT 8
Q4NQH4_9DELT PRELIMINARY; PRT; 188 AA.
ID Q4NQH4_9DELT;
AC Q4NQH4;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Sigma-70 region 2.
GN ORFNames=AdehDRAFT_0950;
OS Anaeromyxobacter dehalogenans 2CP-C.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cytophacteriineae; Myxococcaceae; Anaeromyxobacter.
OX NCBI_TaxID=290397;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=2CP-C;
RC US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hamon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Anaeromyxobacter
RL dehalogenans 2CP-C."
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=2CP-C;
RC US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Anaeromyxobacter
RL dehalogenans 2CP-C."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AAHD0100035; EAL77797.1; -; Genomic DNA.
SQ SEQUENCE 188 AA; 21278 MW; 6DEAFDBF874C4721 CRC64;

Query Match 49.0%; Score 48; DB 2; Length 188;
Best Local Similarity 30.6%; Pred. No. 18;
Matches 11; Conservative 4; Mismatches 3; Indels 18; Gaps 1;

Qy 1 GIRPFLGSI-----WRFIRAFY 18
Db 30 GVRRLGSLVLRDGDADAYARFEESLWRALPAFRG 65

RESULT 9
Q8R587_MOUSE PRELIMINARY; PRT; 298 AA.
ID Q8R587_MOUSE;
AC Q8R587;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
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"A superfamily of XK-related genes (XRG) widely expressed in

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HS25;
RA Pontarollo R.A.;
RL Thesis (1996), V. I. D. O., University of Saskatchewan.
DR EMBL; U28154; AAC45167.1; -, Genomic_DNA.
FT NON_TER 240 240
SQ SEQUENCE 240 AA; 26610 MW; 63348D8619BBAC30 CRC64;

Query Match 48.5%; Score 47.5; DB 2; Length 240;
Best Local Similarity 57.9%; Pred. No. 28;
Matches 11; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Qy 1 GIRFLGSIWRFIR-AFYG 18
||:|||||:|:|:|
Db 201 GTFQFLGGIWEHKEAFNG 219

RESULT 13
Q5U414 XENLA
ID Q5U414 XENLA PRELIMINARY; PRT; 486 AA.
AC Q5U414
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE LOC495492 protein (fragment).
GN Name=LOC495492;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xeropodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RT Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grummond J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smal M.A.;
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Klein S., Gerhard D.S.;
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; BC085081; AAH85081.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.

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DR GO; GO:0005355; F:glucose transporter activity; IEA.
DR GO; GO:0005351; F:sugar porter activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0008643; P:carbohydrate transport; IEA.
DR InterPro; IPR000803; Gluc_transporter.
DR InterPro; IPR007114; MFS_.
DR InterPro; IPR005826; Sub_transporter.
DR InterPro; IPR003663; Sug_transporter.
DR InterPro; IPR005829; Sug_transporter.
DR Pfam; PF00083; Sugar_tr; 1.
DR PRINTS; PR00172; GLUCTRNSPORT.
DR PRINTS; PR00171; SUGTRNSPORT.
DR TIGRfams; TIGR00879; SP; 1.
DR PROSITE; PS00850; MFS; 1.
DR PROSITE; PS00217; SUGAR_TRANSPORT_2; UNKNOWN_1.
DR KW Sugar transport; Transmembrane; Transport.
FT NON_TER 1
SQ SEQUENCE 486 AA; 54035 MW; E333F97CD90A1119 CRC64;

Query Match 48.0%; Score 47; DB 2; Length 486;
Best Local Similarity 50.0%; Pred. No. 70;
Matches 9; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

Qy 1 GIRFLGSIWRFIRAF 16
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Db 174 GLREFLGSETLWPLYMAP 191

RESULT 14
Q5ZDS6 ORYSA
ID Q5ZDS6 ORYSA PRELIMINARY; PRT; 910 AA.
AC Q5ZDS6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative leucyl-tRNA synthetase.
GN Name=P0698A04.32;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22337376; PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikeno M., Ito S., Ito T., Ito Y., Iwabuchi A., Kamiya K.,
RA Karasawa K., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takasaki Y., Terasawa K., Teuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.-I., Eun M.-Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
CC -1- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA (Leu) = AMP +
CC diphosphate + L-leucyl-tRNA(Leu).
DR EMBL; AP002858; BAD52586.1; -, Genomic_DNA.
DR Gramene; Q5ZDS6; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.
DR GO; GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
DR InterPro; IPR002302; Leu-tRNA-synt1a.
DR InterPro; IPR002300; tRNA-synt_1a.
DR InterPro; IPR001412; tRNA-synt_1.
DR Pfam; PF00133; tRNA-synt_1; 1.
DR PRINTS; PR00985; TRNASYNTHLEU.

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DR TIGRFAMs; TIGR00396; leuS_bact; 1.
DR PROSITE; PS00178; AA_TENA_LIGASE_I; 1.
KW ATP-binding; Aminoacyl-tRNA synthetase; Ligase; Nucleotide-binding;
KW Protein biosynthesis.
SQ SEQUENCE 910 AA; 102551 MW; E5856521EC817196 CRC64;
Query Match 48.0%; Score 47; DB 2; Length 910;
Best Local Similarity 53.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GIRFGLGIWRPI 13
: : : : :
Db 722 GVHFLGRTWRLV 734

RESULT 15
Q5ZPA2_9DELT PRELIMINARY; PRT; 385 AA.
AC Q5ZPA2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Angiococcus disciformis.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cystobacterineae; Cystobacteraceae; Cystobacter.
OX NCBI_TaxID=38;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=An d48;
RX PubMed=15324808; DOI=10.1016/j.chembiol.2004.05.014;
RA Sandmann A.; Sasse F.; Mueller R.;
RT "Identification and analysis of the core biosynthetic machinery of
RT tubulysin, a potent cytotoxin with potential anticancer activity.";
RL Chem. Biol. 11:1071-1079(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=An d48;
RA Sandmann A.;
RT "Identifizierung und Charakterisierung des Tubulysin
RT Biosynthesegencusters aus dem Myxobakterium Angiococcus disciformis
RT An d48.";
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ620477; CAF05655.1; -; Genomic_DNA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR006025; Rept_M_Zn_BS.
DR SMART; SM00247; XTALbg; 1.
DR PROSITE; PS0915; CRYSTALLIN_BETAGAMMA; 2.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 385 AA; 43283 MW; CE609F2D64027CA0 CRC64;

Query Match 46.9%; Score 46; DB 2; Length 385;
Best Local Similarity 42.9%; Pred. No. 80;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 5 FLGSIWRIFAFYG 18
: : : : :
Db 66 YLGDVWRYTKRTYG 79

Search completed: March 29, 2006, 01:49:11
Job time : 168.938 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 29, 2006, 01:49:32 ; Search time 37.6875 Seconds
(without alignments)
39.487 Million cell updates/sec

Title: US-10-712-447-5

Perfect score: 98

Sequence: 1 GIRFLGSIWIRAFYQ 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5 COMB.pap:*
- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pap:*
- 3: /cgn2_6/ptodata/1/iaa/H COMB.pap:*
- 4: /cgn2_6/ptodata/1/iaa/PTUS COMB.pap:*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pap:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	79.6	18	2	US-08-940-095-242 Sequence 242, App
2	78	79.6	18	2	US-08-940-093-242 Sequence 242, App
3	78	79.6	18	2	US-08-940-096-242 Sequence 242, App
4	78	79.6	18	2	US-09-465-719-242 Sequence 242, App
5	78	79.6	18	2	US-09-453-605-242 Sequence 242, App
6	78	79.6	18	2	US-09-453-838-242 Sequence 242, App
7	78	79.6	18	2	US-08-940-136-242 Sequence 242, App
8	78	79.6	18	2	US-09-453-841-242 Sequence 242, App
9	78	79.6	18	2	US-09-453-833-242 Sequence 242, App
10	78	79.6	18	2	US-09-453-826-242 Sequence 242, App
11	78	79.6	18	2	US-09-453-840-242 Sequence 242, App
12	78	79.6	18	2	US-09-865-989-242 Sequence 242, App
13	78	79.6	18	2	US-09-453-834-242 Sequence 242, App
14	78	79.6	18	2	US-10-283-599-242 Sequence 242, App
15	78	79.6	18	2	US-09-465-718-242 Sequence 242, App
16	51	52.0	76	2	US-09-205-258-892 Sequence 892, App
17	51	52.0	76	2	US-10-004-860-892 Sequence 892, App
18	47.5	48.5	253	2	US-09-586-106D-49 Sequence 49, Appl
19	47.5	48.5	253	2	US-10-799-870-49 Sequence 49, Appl
20	45.5	46.4	254	2	US-09-586-106D-45 Sequence 45, Appl
21	45.5	46.4	254	2	US-10-799-870-45 Sequence 45, Appl
22	45	45.9	22	1	US-08-338-882-40 Sequence 40, Appl
23	45	45.9	22	1	US-08-338-882-41 Sequence 41, Appl
24	45	45.9	539	2	US-09-710-279-340 Sequence 340, App
25	45	45.9	835	2	US-09-134-001C-5105 Sequence 5105, App
26	45	45.9	877	2	US-09-328-352-8162 Sequence 8162, App
27	44	44.9	22	1	US-08-132-767-50 Sequence 50, Appl

28	44	44.9	589	1	US-08-756-317-5	Sequence 5, Appli
29	44	44.9	1052	2	US-09-134-000C-6620	Sequence 6620, Ap
30	43	43.9	23	2	US-10-360-101-83	Sequence 83, Appl
31	43	43.9	683	2	US-09-902-1540-15932	Sequence 15932, A
32	43	43.9	812	2	US-09-538-092-643	Sequence 643, App
33	42	42.9	14	1	US-08-480-190-3	Sequence 3, Appli
34	42	42.9	14	1	US-08-488-379-3	Sequence 3, Appli
35	42	42.9	14	2	US-08-475-399A-3	Sequence 3, Appli
36	42	42.9	14	2	US-08-077-255A-3	Sequence 3, Appli
37	42	42.9	14	4	PCT-US93-07545-3	Sequence 2, Appli
38	42	42.9	15	1	US-08-480-190-2	Sequence 2, Appli
39	42	42.9	15	1	US-08-488-379-2	Sequence 2, Appli
40	42	42.9	15	2	US-08-475-399A-2	Sequence 2, Appli
41	42	42.9	15	2	US-08-077-255A-2	Sequence 2, Appli
42	42	42.9	15	4	PCT-US93-07545-2	Sequence 2, Appli
43	42	42.9	18	1	US-08-480-190-1	Sequence 1, Appli
44	42	42.9	18	1	US-08-480-190-61	Sequence 61, Appli
45	42	42.9	18	1	US-08-488-379-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-940-095-242
; Sequence 242, Application US/08940095
; Patent No. 6004925
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DISLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,095
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/POCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6004925e
US-08-940-095-242

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Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GRRFLGSIWRFIRAFYG 18
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Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 2
US-08-940-093-242
; Sequence 242, Application US/08940093
; Patent No. 6037323
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,093
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6037323e
; US-08-940-093-242

Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GRRFLGSIWRFIRAFYG 18
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Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 3
US-08-940-096-242
; Sequence 242, Application US/08940096
; Patent No. 6046166
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
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; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,096
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6046166e
; US-08-940-096-242

Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GRRFLGSIWRFIRAFYG 18
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Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 4
US-09-465-719-242
; Sequence 242, Application US/09465719
; Patent No. 6265377
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/465.719
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,093
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6265377e
US-09-465-719-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFVG 18
||:|||||:|:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 5
US-09-453-605-242
; Sequence 242, Application US/09453605
; Patent No. 6329341
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,605
; FILING DATE: 26-No. 6329341-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6329341e
SEQUENCE DESCRIPTION: SEQ ID NO: 242:
US-09-453-605-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFVG 18
||:|||||:|:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 6
US-09-453-838-242
; Sequence 242, Application US/09453838
; Patent No. 6376464
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
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; APPLICATION NUMBER: US/09/453,838
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6376464e
; US-09-453-838-242

RESULT 8
US-09-453-841-242
; Sequence 242, Application US/09453841

RESULT 8
US-09-453-841-242
; Sequence 242, Application US/09453841

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; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,833
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-5556
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6630450e
; US-09-453-826-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRFLGSIWRFIRAFVG 18
   ||::|||::|||::|||
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 11
US-09-453-840-242
; Sequence 242, Application US/09453840
; Patent No. 6716816
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttnr, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,840
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid

; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,826
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-5556
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6716816e
US-09-453-840-242

Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRPIAFVG 18
|::|::|::|::|::|::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 12
US-09-865-989-242
; Sequence 242, Application US/09865989
; Patent No. 6734169
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 09/465,719
; FILING DATE: 17-DEC-1999
; PRIOR APPLICATION NUMBER: 09/465,719
; FILING DATE: 25-MAY-2001
; CLASSIFICATION: <Unknown>
; APPLICATION NUMBER: 09/465,719
; FILING DATE: 17-DEC-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6734169e
; SEQUENCE DESCRIPTION: SEQ ID NO: 242:

US-09-865-989-242

Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRPIAFVG 18
|::|::|::|::|::|::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 13
US-09-453-834-242
; Sequence 242, Application US/09453834
; Patent No. 6753313
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,834
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6753313e
; US-09-453-834-242

Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRPIAFVG 18
|::|::|::|::|::|::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 14
US-10-283-599-242
; Sequence 242, Application US/10283599
; Patent No. 6844327
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
; USE TO TREAT DYSLIPIDEMIC DISORDERS.
```

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;
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,599
; FILING DATE: 29-OCT-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,136
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0007-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-5556
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6844327e
; US-10-283-599-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFVG 18
|::|::|::|::|::|
Db 1 GIKKFLGSIWKFIRAFVG 18

RESULT 15
US-09-465-718-242
; Sequence 242, Application US/09465718
; Patent No. 6900177
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/465,718
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; FILING DATE: 17-Dec-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,096
; FILING DATE: 29-SEP-1997
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6900177e
; US-09-465-718-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFVG 18
|::|::|::|::|::|
Db 1 GIKKFLGSIWKFIRAFVG 18

Search completed: March 29, 2006, 01:51:15
Job time : 38.6875 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 29, 2006, 02:05:02 ; Search time 153 Seconds
(without alignments)
49.156 Million cell updates/sec

Title: US-10-712-447-5

Perfect score: 98

Sequence: 1 GIRRFLGSIWRFIRAFYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	18	4	US-10-712-447-2
2	98	100.0	18	4	US-10-712-447-5
3	98	100.0	18	4	US-10-712-447-8
4	98	100.0	18	4	US-10-712-447-10
5	98	100.0	18	4	US-10-712-447-13
6	95	96.9	18	4	US-10-712-447-91
7	94	95.9	18	4	US-10-712-447-115
8	94	95.9	18	4	US-10-712-447-116
9	94	95.9	18	4	US-10-712-447-117
10	94	95.9	18	4	US-10-712-447-129
11	94	95.9	18	4	US-10-712-447-131
12	92	93.9	18	4	US-10-712-447-21
13	92	93.9	18	4	US-10-712-447-53
14	92	93.9	18	4	US-10-712-447-74
15	90	91.8	18	4	US-10-712-447-4
16	90	91.8	18	4	US-10-712-447-127
17	89	90.8	18	4	US-10-712-447-99
18	88	89.8	18	4	US-10-712-447-18
19	88	89.8	18	4	US-10-712-447-112
20	88	89.8	18	4	US-10-712-447-113
21	88	89.8	18	4	US-10-712-447-114
22	87	88.8	18	4	US-10-712-447-17
23	86	87.8	18	4	US-10-712-447-61
24	86	87.8	18	4	US-10-712-447-82
25	85	86.7	18	4	US-10-712-447-16
26	85	86.7	18	4	US-10-712-447-96
27	85	86.7	18	4	US-10-712-447-121

28 84 85.7 18 4 US-10-712-447-22 Sequence 22, Appl
29 84 85.7 18 4 US-10-712-447-78 Sequence 78, Appl
30 84 85.7 18 4 US-10-712-447-95 Sequence 95, Appl
31 84 85.7 18 4 US-10-712-447-120 Sequence 120, Appl
32 82 83.7 18 4 US-10-712-447-19 Sequence 19, Appl
33 82 83.7 18 4 US-10-712-447-56 Sequence 56, Appl
34 82 83.7 18 4 US-10-712-447-58 Sequence 58, Appl
35 82 83.7 18 4 US-10-712-447-77 Sequence 77, Appl
36 82 83.7 18 4 US-10-712-447-79 Sequence 79, Appl
37 82 83.7 18 4 US-10-712-447-80 Sequence 80, Appl
38 82 83.7 18 4 US-10-712-447-94 Sequence 94, Appl
39 81 82.7 18 4 US-10-712-447-57 Sequence 57, Appl
40 81 82.7 18 4 US-10-712-447-100 Sequence 100, Appl
41 80 81.6 18 4 US-10-712-447-41 Sequence 41, Appl
42 79 80.6 18 4 US-10-712-447-97 Sequence 97, Appl
43 78 79.6 18 3 US-09-865-989-242 Sequence 242, App
44 78 79.6 18 3 US-09-865-989-242 Sequence 242, App
45 78 79.6 18 4 US-10-099-574A-242 Sequence 242, App

ALIGNMENTS

RESULT 1

US-10-712-447-2
; Sequence 2, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: c-term amidated
US-10-712-447-2

Query Match 100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18
|||||
Db 1 GIRRFLGSIWRFIRAFYG 18
|||||

RESULT 2

US-10-712-447-5
; Sequence 5, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13

; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-5

Query Match 100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18
Db 1 GIRRFLGSIWRFIRAFYG 18
|||||

RESULT 3
US-10-712-447-8
; Sequence 8, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-8

Query Match 100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18
Db 1 GIRRFLGSIWRFIRAFYG 18
|||||

RESULT 4
US-10-712-447-10
; Sequence 10, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210

; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-10

Query Match 100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18
Db 1 GIRRFLGSIWRFIRAFYG 18
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RESULT 5
US-10-712-447-13
; Sequence 13, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-13

Query Match 100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18
Db 1 GIRRFLGSIWRFIRAFYG 18
|||||

RESULT 6
US-10-712-447-91
; Sequence 91, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 91
; LENGTH: 18

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RESULT 10
US-10-712-447-129
; Sequence 129, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 129
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-129

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Query Match      95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.5e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFLRAFYG 18
    |||||:|||||
Db 1 GIRRFLGSIWRFLRAFYG 18
    |||||:|||||

RESULT 11
US-10-712-447-131
; Sequence 131, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 131
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-712-447-131

Query Match      95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.5e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFLRAFYG 18
    |||||:|||||
Db 1 GIRRFLGSIWRFLRAFYG 18
    |||||:|||||

RESULT 12
US-10-712-447-21
; Sequence 21, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 21
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-712-447-21

Query Match      93.9%; Score 92; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 7.1e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFLRAFYG 18
    |||||:|||||
Db 1 GIRRFLGSIWRFLRAFYG 18
    |||||:|||||

RESULT 13
US-10-712-447-53
; Sequence 53, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 53
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-712-447-53

Query Match      93.9%; Score 92; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 7.1e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFLRAFYG 18
    |||||:|||||
Db 1 GIRRFLGSIWRFLRAFYG 18
    |||||:|||||

RESULT 14
US-10-712-447-74
; Sequence 74, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 74
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-712-447-74
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Wed Mar 29 18:01:20 2006

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; OTHER INFORMATION: peptide
US-10-712-447-74
Query Match          93.9%; Score 92; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 7.1e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18
   |||:|||:|||:|||
Db  1 GIRRFLGSIWRFIRAFYG 18

RESULT 15
US-10-712-447-4
; Sequence 4, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-4
Query Match          91.8%; Score 90; DB 4; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.4e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18
   |||:|||:|||:|||
Db  1 GIRRFLGSIWRFIRAFVG 18

Search completed: March 29, 2006, 02:10:39
Job time : 153 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 29, 2006, 02:06:17 ; Search time 16.875 Seconds

(without alignments)
31.461 Million cell updates/sec

Title: US-10-712-447-5

Perfect score: 98

Sequence: 1 GIRFLGSINWFIRAFVG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174695 seqs, 29494374 residues

Total number of hits satisfying chosen parameters: 174695

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /SIDSS/ptodata/1/pubpaa/US08 NEW PUB.pap.*
- 2: /SIDSS/ptodata/1/pubpaa/US06 NEW PUB.pap.*
- 3: /SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pap.*
- 4: /SIDSS/ptodata/1/pubpaa/PCT_NEW PUB.pap.*
- 5: /SIDSS/ptodata/1/pubpaa/US09 NEW PUB.pap.*
- 6: /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pap.*
- 7: /SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pap.*
- 8: /SIDSS/ptodata/1/pubpaa/US60_NEW PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	45.9	306	7	US-11-096-568A-16673
2	45	45.9	327	7	US-11-096-568A-16672
3	45	45.9	360	7	US-11-096-568A-16671
4	45	45.9	539	6	US-10-793-626-340
5	44	44.9	379	5	US-09-978-360A-506
6	42	42.9	85	7	US-11-172-740-229
7	42	42.9	365	6	US-10-821-234-1575
8	42	42.9	805	6	US-10-485-517-198
9	41	41.8	265	6	US-10-392-234A-54
10	41	41.8	394	7	US-11-087-099-521
11	41	41.8	394	7	US-11-087-099-1491
12	41	41.8	394	7	US-11-087-099-1644
13	41	41.8	394	7	US-11-087-099-1700
14	41	41.8	394	7	US-11-087-099-2589
15	41	41.8	394	7	US-11-087-099-2733
16	41	41.8	394	7	US-11-087-099-3648
17	41	41.8	394	7	US-11-087-099-4073
18	41	41.8	394	7	US-11-087-099-4652
19	41	41.8	394	7	US-11-087-099-4677
20	41	41.8	394	7	US-11-087-099-4777
21	41	41.8	394	7	US-11-087-099-4910
22	41	41.8	394	7	US-11-087-099-6008
23	41	41.8	394	7	US-11-087-099-6227
24	41	41.8	394	7	US-11-087-099-6781
25	41	41.8	394	7	US-11-087-099-6911

ALIGNMENTS

RESULT 1

US-11-096-568A-16673
; Sequence 16673, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 16673
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(306)
; OTHER INFORMATION: Ceres Seq. ID no. 12353656
US-11-096-568A-16673

Query Match 45.9%; Score 45; DB 7; Length 306;
Best Local Similarity 58.3%; Pred. No. 5.6;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IRRFLGSINWF 13
DB 200 VRESLGSINWRF 211

RESULT 2

US-11-096-568A-16672
; Sequence 16672, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 16672
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:

Sequence 7139, Ap
Sequence 7287, Ap
Sequence 7806, Ap
Sequence 7928, Ap
Sequence 8706, Ap
Sequence 8837, Ap
Sequence 9004, Ap
Sequence 9271, Ap
Sequence 9973, Ap
Sequence 10104, A
Sequence 10325, A
Sequence 10517, A
Sequence 11001, A
Sequence 11036, A
Sequence 11514, A
Sequence 11905, A
Sequence 12199, A
Sequence 12453, A
Sequence 6018, Ap
Sequence 26625, A

; NAME/KEY: misc feature
; LOCATION: (1)..(327)
; OTHER INFORMATION: Ceres Seq. ID no. 12353655
US-11-096-568A-16672

Query Match 45.9%; Score 45; DB 7; Length 327;
Best Local Similarity 58.3%; Pred. No. 6;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IRRFLGSIWRPI 13
:| |||:|
Db 221 VRESLGLWRPM 232

RESULT 3
US-11-096-568A-16671
; Sequence 16671, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 16671
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(360)
; OTHER INFORMATION: Ceres Seq. ID no. 12353654
US-11-096-568A-16671

Query Match 45.9%; Score 45; DB 7; Length 360;
Best Local Similarity 58.3%; Pred. No. 6.5;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IRRFLGSIWRPI 13
:| |||:|
Db 254 VRESLGLWRPM 265

RESULT 4
US-10-793-626-340
; Sequence 340, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793.626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 340
; LENGTH: 539
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-340

Query Match 45.9%; Score 45; DB 6; Length 539;
Best Local Similarity 61.5%; Pred. No. 9.6;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIRFLGSIWRPI 13

Db 357 GSRFLDRVRLI 369
| |||:| |

RESULT 5
US-09-978-360A-506
; Sequence 506, Application US/09978360A
; Publication No. US20060009633A9
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56.US4.CIP
; CURRENT APPLICATION NUMBER: US/09/978,360A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: -09-04
; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/215,435
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/IB98/02122
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; PRIOR FILING DATE: 1999-02-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent.pm
; SEQ ID NO 506
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -37..-1
US-09-978-360A-506

Query Match 44.9%; Score 44; DB 5; Length 379;
Best Local Similarity 53.3%; Pred. No. 9.9;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 RFLGSIWRFIAPFYG 18
:| |||:|
Db 76 RYRGSIWRIVRACLG 90

RESULT 6
US-11-172-740-229
; Sequence 229, Application US/11172740
; Publication No. US20060057724A1
; GENERAL INFORMATION:
; APPLICANT: MASCIA, Peter
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR
; TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
; FILE REFERENCE: 2750-1602PUS2
; CURRENT APPLICATION NUMBER: US/11/172,740
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,621


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; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/584,829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/584,800
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 2523
; SEQ ID NO 229
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13)..(81)
; OTHER INFORMATION: Pfam Name: PC4; Pfam Description: Transcriptional Coactivator p15
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for delaying flowering time
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making lethal plants for genetic confinement
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making ornamental plants with modified flower
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making plants sterile and for genetic confine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making plants with increased biomass and fold
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making smaller plants
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making taller plants and plants with longer
; OTHER INFORMATION: inflorescences
US-11-172-740-229

Query Match 42.9%; Score 42; DB 7; Length 85;
Best Local Similarity 50.0%; Pred. No. 5.1;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 2 IRRFLGSIWRFIRAFY 17
Db 54 VRNNGKIWDIREFY 69

RESULT 7
US-10-821-234-1575
; Sequence 1575, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1575
; LENGTH: 365
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1575

Query Match 42.9%; Score 42; DB 6; Length 365;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 6 LGSIWRFIRAFY 17
Db 127 VGSDWRFRLRGVH 138

RESULT 8
US-10-485-517-198
; Sequence 198, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629W0
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 198
; LENGTH: 805
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-198

Query Match 42.9%; Score 42; DB 6; Length 805;
Best Local Similarity 53.8%; Pred. No. 43;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFPI 13
Db 623 GSRFRFLDRVWRLM 635

RESULT 9
US-10-392-234A-54
; Sequence 54, Application US/10392234A
; Publication No. US2005025538A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia and Upjohn Corporation
; APPLICANT: Buxser, Steven
; APPLICANT: Poole, Keith
; APPLICANT: Decker, Douglas
; APPLICANT: Xiazunhi Li
; TITLE OF INVENTION: Method for Screening for acraB Transporter Family Inhibitors
; FILE REFERENCE: 6206
; CURRENT APPLICATION NUMBER: US/10/392,234A
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US 60/364,935
; PRIOR FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-392-234A-54

Query Match 41.8%; Score 41; DB 6; Length 265;
Best Local Similarity 50.0%; Pred. No. 22;
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Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 9 IWREIRAFYG 18
||||: :||
Db 223 IWREMKVYFG 232

RESULT 10

US-11-087-099-521
; Sequence 521, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 521
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-11-087-099-521

Query Match 41.8%; Score 41; DB 7; Length 394;
Best Local Similarity 54.5%; Pred. No. 31;
Matches 6; Conservative 3; Mismatches 0; Gaps 0;

Qy 6 LGSIWRFIRAF 16
:|:|:|:
Db 19 VGGWMAFLRAF 29

RESULT 11

US-11-087-099-1491
; Sequence 1491, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1491
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(394)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-087-099-1491

Query Match 41.8%; Score 41; DB 7; Length 394;
Best Local Similarity 54.5%; Pred. No. 31;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 LGSIWRFIRAF 16
:|:|:|:
Db 19 VGGWMAFLRAF 29

RESULT 12

US-11-087-099-1644
; Sequence 1644, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22

; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1644
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-11-087-099-1644

Query Match 41.8%; Score 41; DB 7; Length 394;
Best Local Similarity 54.5%; Pred. No. 31;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 LGSIWRFIRAF 16
:|:|:|:
Db 19 VGGWMAFLRAF 29

RESULT 13

US-11-087-099-1700
; Sequence 1700, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1700
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-11-087-099-1700

Query Match 41.8%; Score 41; DB 7; Length 394;
Best Local Similarity 54.5%; Pred. No. 31;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 LGSIWRFIRAF 16
:|:|:|:
Db 19 VGGWMAFLRAF 29

RESULT 14

US-11-087-099-2589
; Sequence 2589, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 2589
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-11-087-099-2589

Query Match 41.8%; Score 41; DB 7; Length 394;
Best Local Similarity 54.5%; Pred. No. 31;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 LGSIWRFIRAF 16
:|:|:|:
Db 19 VGGWMAFLRAF 29

RESULT 15

US-11-087-099-2733
; Sequence 2733, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:

Wed Mar 29 18:01:21 2006

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; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 2733
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-11-087-099-2733

Query Match      41.8%; Score 41; DB 7; Length 394;
Best Local Similarity 54.5%; Pred. NO. 31;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      6 LGSIWRFIRAF 16
       :|:|:|:|
Db      19 VGGMWAFLRAF 29
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Search completed: March 29, 2006, 02:11:16
Job time : 17.875 secs

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